Access DB# ___

TEXT 102949

Scientific and Technical Information Center

CRFE

Requester's Full Name: BAO – Art Unit: 1641 Phone N Mail Box and Bldg/Room Location	THUY NGUYE Number 30 <u>8 - 42</u> n: 7 <u>E05</u> Rea	A/Examiner # :	73 403 Date: 8/27 nber: 09/830,87 rred (circle): PAPER DIS	1/03 7∕ <u>6</u> SK E-MAIL
If more than one search is subm ***************************** Please provide a detailed statement of the. Include the elected species or structures, k utility of the invention. Define any terms known. Please attach a copy of the cover s	****************** search topic, and describe eywords, synonyms, acro that may have a special n	************ e as specifically as poornyms, and registry nuneaning. Give examp	************************** ssible the subject matter to be ambers, and combine with the	concept or
Title of Invention:			·	
Inventors (please provide full names):	JOHN H. S	KERRITT		
Earliest Priority Filing Date:	11111998			
For Sequence Searches Only Please includ appropriate serial number.	de all pertinent information	(parent, child, division	al, or issued patent numbers) alo	ng with the
. Please search an	tibody th	at bind	to SEQ ID	1-3
of alpha-amylo	ase	and the		
- Inventor				
AA 15		, similar	hank you	·
7-10				
	×*	•		(1)
************	******	******	*******	****
STAFF USE ONLY	Type of Search	4	and cost where applicable	
Searcher: 1 4 Searcher Phone #:	NA Sequence (#)	STN	2 3 8	
Searcher Phone #:	AA Sequence (#) Structure (#)	Dialog		 _
Date Searcher Picked Up:	Bibliographic	Dr.Link		
Date Completed:	Litigation	Lexis/Nexis_		
Searcher Prep & Review Time: SEQ:8 57NZ		Sequence Systems	02	
Clerical Prep Time:	Patent Family	WWW/Internet		
Online Time: Seg. 8 ST A . 1.7	Other	Other (specify)		
PTO-1590 (8-01)	101		·	



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

/o	luntary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
A	Relevant prior art found, search results used as follows: 102 rejection 103 rejection Cited as being of interest. Helped examiner better understand the invention. Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found: Foreign Patent(s) Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found: Results verified the lack of relevant prior art (helped determine patentability). Results were not useful in determining patentability or understanding the invention.
Coi	mments:

Propolitor send completed forms to STIC/Biotech:Chem/Library GMil = Circ ; Desk



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=> d his
      (FILE 'HOME' ENTERED AT 11:12:37 ON 03 SEP 2003)
      FILE 'CAPLUS' ENTERED AT 11:12:46 ON 03 SEP 2003
             207 S SKERRITT J?/AU
L2
              69 S L1 AND (CEREAL OR GRAIN)
           17614 S ALPHA-AMYLASE OR .ALPHA.AMYLASE OR .ALPHA. AMYLASE
L3
              3 S L2 AND L3 4 related to instant application
53 S L2 AND ANTIBOD? > includes L4 cites
L4
     FILE 'REGISTRY' ENTERED AT 11:17:41 ON 03 SEP 2003
               65 E1-6 6 cpds from L4 cites
L6
     FILE 'CAPLUS' ENTERED AT 11:18:52 ON 03 SEP 2003
      FILE 'REGISTRY' ENTERED AT 11:19:24 ON 03 SEP 2003
               4 S L6 NOT CL/ELS & getting rid of call salts
L7
     FILE 'CAPLUS' ENTERED AT 11:19:53 ON 03 SEP 2003

3 S L7 AND L4 3 cites w/ 4

51 S L5 NOT L4 5/ cites
                                                            cpds d
L8
     FILE 'REGISTRY' ENTERED AT 11:21:39 ON 03 SEP 2003

1 S IDALVSIRTRGOIHS/SQSP ( Sep ID 1)

35 S CRDDRPYADG/SQSP ( Sep ID 2)

7 S VNWVNKVGGS/SQSP ( Sep ID 3)
                                                                    searched as exact ; embedded sequences
L10
L11
L12
     FILE 'CAPLUS' ENTERED AT 11:24:50 ON 03 SEP 2003
1 S L10
L13
L14
               5 S L11
               3 S L12
L15
               1 S L13-15 AND ANTIBOD? I cite mention S anti bu dies
     FILE 'USPATFULL' ENTERED AT 11:25:44 ON 03 SEP 2003
               0 S L10
L17
               0 S L11
L18
119
               0 S L12
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FILE 'CAPLUS' ENTERED AT 11:26:03 ON 03 SEP 2003

=> d sqide 17

LC

L7 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 268202-96-6 REGISTRY
CN L-Serine, L-valyl-L-asparaginyl-L-tryptophyl-L-valyl-L-asparaginyl-L-lysyl-L-valylglycylglycyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 10

SEQ 1 VNWVNKVGGS
MF C47 H74 N14 014
SR CA

Absolute stereochemistry.

STN Files: CA, CAPLUS

1 REFERENCES IN FILE CA'(1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d sqide 17 2

L7 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 268202-95-5 REGISTRY
CN Glycine, L-cysteinyl-L-arginyl-L-alpha.-aspartyl-L-arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-alpha.-aspartyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
10
SEQ 1 CRDDRPYADG
C46 H70 N16 O18 S
SR CA
LC STN Files: CA, CAPLUS

Absolute stereochemistry.

PAGE 2-A

1 REFERENCES IN FILE CA (1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d sqide 17 3

- ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN 268202-94-4 REGISTRY L7
- RN
- L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-CN L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutaminyl-L-isoleucyl-L-histidyl- (9CI) (CA INDEX NAME) PROTEIN SEQUENCE; STEREOSEARCH
- SQL
- 1 IDALVSIRTR GQIHS
- MF C71 H124 N24 O22
- SR CA
- STN Files: LC CA, CAPLUS

Absolute stereochemistry.

PAGE 1-A

PAGE 2-A

PAGE 2-B

Мe

PAGE 3-A

1 REFERENCES IN FILE CA (1937 TO DATE) 1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d 17 4

ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN 9000-90-2 REGISTRY L7

RN

Amylase, .alpha.- (9CI) (CA INDEX NAME)

Searched by Susan Hanley 305-4053

```
OTHER NAMES:
      .alpha.-Amylase
      1,4-.alpha.-D-Glucan glucanohydrolase
     1,4-.alpha.-D-Glucanase
CN
     1,4-.alpha.-Glucanase
CN
     Amano AD 1
CN
CN
     Amylase AD
     Amylase THC 250
CN
     Amylogal CS
CN
     Amylolisin 5
CN
CN
     Amylopsin
     Amylosubtilin
CN
CN
     Aquazym 120L
CN
      Aquazyme 240
CN
      Bactosol TK
CN
     Ban
CN
CN
      Ban (enzyme)
      BAN 120L
      BAN 240
CN
      Ban 480L
CN
      Beisol T 2090
CN
      Biobake 40000
CN
      Bioferm
CN
      Bioferm P
CN
CN
      Bioprep TBS
      Biotex GT
CN
      Biozyme A
CN
      Biozyme F
      Brewers Amylique TS
CN
CN
      Buclamase
      Canalpha 1000P
CN
CN
      Canalpha 600L
      Canalpha 60P
CN
CN
      Clarase
      Denazyme SA 7
CN
CN
      Desize 160
CN
      E.C. 3.2.1.1
CN
      Ekikakoso 6T
      EMCEmaltex 1000
CN
CN
      Endoamylase
CN
      FD Super
      Fortizyme
CN
CN
      Fungamyl
      Fungamyl 2500BG
CN
CN
      Fungamyl 300L
      Fungamyl 800L
CN
CN
      G 995
      G-zyme G 995
CN
CN
      G6-Amylase
      Gamalpha HT 120L
CN
      Gemsize 4A
.CN
ADDITIONAL NAMES NOT AVAILABLE IN THIS FORMAT - Use FCN, FIDE, or ALL for
      9000-85-5, 152923-47-2, 152923-48-3, 152923-49-4
      9001-95-0, 9036-05-9, 9077-78-5, 135319-50-5, 106009-10-3, 70356-39-7,
DR
      144133-13-1
MF
      Unspecified
      COM, MAN
CI
      STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,
        CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM, CSNB, DDFU, DIOGENES, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, MRCK*, MSDS-OHS, NAPRALERT, NIOSHTIC, PHARMASEARCH, PIRA, PROMT, RTECS*,
        TOXCENTER, USAN, USPAT2, USPATFULL
      (*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
           (**Enter CHEMLIST File for up-to-date regulatory information)
```

NGUYEN 09/830,876

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

13729 REFERENCES IN FILE CA (1937 TO DATE)

207 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
13740 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d ibib abs hitrn 18 1-3

```
ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                           2002:53744
                                        CAPLUS
DOCUMENT NUMBER:
                           137:120380
TITLE:
                           Albumin polymorphism and mapping of a dimeric .
                           alpha.-amylase inhibitor in wheat
AUTHOR(S):
                           Singh, J.; Appels, R.; Sharp, P. J.; Skerritt, J.
CORPORATE SOURCE:
                           Cooperative Research Centre for Quality Wheat Products
                           and Processes, North Ryde, NSW 2113, Australia
SOURCE:
                           Australian Journal of Agricultural Research (2001),
                           52(11&12), 1173-1179
                           CODEN: AJAEA9; ISSN: 0004-9409
                           CSIRO Publishing
PUBLISHER:
DOCUMENT TYPE:
                           Journal
LANGUAGE:
                           English
     Any new protein or DNA marker is potentially useful to add detail to
     already constructed genetic chromosome maps and may be valuable in
     breeding programs wherever polymorphism exists. Non-gluten proteins
     represent 15-20% of total wheat grain proteins. Isoelec.
     focusing of wheat (Triticum aestivum L. em Thell.) proteins on ultrathin gels showed high resoln. and was found to be a useful tool in the
     differentiation of wheat varieties. Seventeen hexaploid wheat varieties
     were screened to investigate polymorphism of albumin proteins using
     isoelec. focusing. Polymorphism was obsd. for albumin polypeptides of pI 5.20, 5.85, 6.25, and 7.1, and 8.0. The polymorphic protein of pl 7.1 was mapped by analyzing doubled haploid populations from the intervarietal
     crosses, Cranbrook Halberd and Synthetic Opata 85. This protein locus
     was designated as Iha-B1.2, and is located on the short arm of chromosome
TT
     9000-90-2, .alpha.-Amylase
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (inhibitor WDA1-3; albumin polymorphisms and mapping of dimeric
         .alpha.-amylase inhibitor WDA1-3 in wheat using
         isoelec. focusing)
REFERENCE COUNT:
                                  THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS
                                  RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
    ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                           2000:335649
                                         CAPLUS
DOCUMENT NUMBER:
                           132:333681
TITLE:
                           Detection of preharvest sprouting in cereal
                           grains by immunoassay of alpha.
                           amvlase
INVENTOR(S):
                           Skerritt, John Howard
                           Quality Wheat CRC Limited, Australia
PATENT ASSIGNEE(S):
                           PCT Int. Appl., 51 pp.
SOURCE:
                           CODEN: PIXXD2
DOCUMENT TYPE:
                           Patent
LANGUAGE:
                           English
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                        KIND DATE
                                               APPLICATION NO. DATE
     WO 2000028319
                        Α1
                              20000518
                                               WO 1999-AU995
                                                                 19991111
         W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
              PT, SE
                                               CA 1999-2345403 19991111
     CA 2345403
                         AA
                              20000518
     EP 1137935
                                               EP 1999-957719 19991111
                         Α1
                              20011004
         R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, FI
     JP 2002529735
                         T2
                              20020910
                                               JP 2000-581446
                                                                 19991111
     AU 757926
                                               AU 2000-15341
                              20030313
                         B2
                                                                 19991111
PRIORITY APPLN. INFO.:
                                            AU 1998-7058
                                                              A 19981111
```

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WO 1999-AU995
                                                               W 19991111
     A two-site immunoassay for the qual. or quant. detection of .alpha
     .-amylase in a test sample comprises: (i) exposing the test
     sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .
     alpha.-amylase under conditions permitting binding; (ii)
     subsequently exposing bound .alpha.-amylase to a
     second ("detection") antibody or antibody fragment which specifically or
     preferentially binds to a second epitope on the .alpha.-
     amylase that is distinct from the first epitope, under conditions
     permitting binding of the second antibody or its fragment to the bound .
     alpha.-amylase; and (iii) detecting any binding of the
     second antibody or its fragment to the bound .alpha.-
     amylase, wherein either of the first or second epitopes is an
     epitope comprising one or more of the amino acid sequences:
     IDRLVSIRTRGQIHS, CRDDRPYADG, or VNWVNKVGGS and variants thereof showing
      .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay
     is useful for detecting weather damage (i.e., preharvest sprouting) in
     cereal grain. Thus, a rapid tube sandwich ELISA
     detected .alpha.-amylase in preharvest-sprouted wheat
     exts. at .apprx.4 ng/mL.
     9000-90-2, .alpha.-Amylase 268202-94-4
268202-95-5 268202-96-6
     RL: ANT (Analyte); ANST (Analytical study)
         (detection of preharvest sprouting in cereal grains
         by immunoassay of .alpha.-amylase)
REFERENCE COUNT:
                                  THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
                           3
                                  RECORD, ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 3. OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                            1999:636830 CAPLUS
DOCUMENT NUMBER:
                            131:335982
TITLE:
                            Development of a field enzyme-linked immunosorbent
                            assay (ELISA) for detection of .alpha.-
                            amylase in preharvest-sprouted wheat
AUTHOR(S):
                            Verity, J. Christiana K.; Hac, Luch; Skerritt,
CORPORATE SOURCE:
                            Quality Wheat CRC Ltd. and CSIRO Plant Industry,
                            Canberra, ACT 2601, Australia
SOURCE:
                            Cereal Chemistry (1999), 76(5), 673-681
                            CODEN: CECHAF; ISSN: 0009-0352
                            American Association of Cereal Chemists
PUBLISHER:
DOCUMENT TYPE:
                            Journal
LANGUAGE:
                           English
     A sandwich ELISA was developed for detection of .alpha.-
     amylase in preharvest sprouted wheat and adapted to rapid
     field-use formats requiring 15-20 min to perform. Polyclonal and
     monoclonal antibodies were prepd. to detect a mixt. of high and low pI isoenzymes of .alpha.-amylase and high pI isoenzymes
     only. All antibodies detected .alpha.-amylase on
     immunoblots of either a crude wheat ext. or of purified enzyme, but only
     the polyclonal antibodies functioned in a sandwich ELISA. Depending on
     the antibody combination, the tube ELISA detected either the high and low
     pI isoenzymes of .alpha.-amylase or the high pI
     isoenzymes only with a detection limit of .apprxeq.0.5-1.0 ng/mL of amylase. Wheats with falling nos. (FN) of <350 s could be discriminated from sound wheats, with decreasing FN producing increasing assay color.
     Using 130 wheat grain samples, ELISA absorbances for detection
     of both high and low pl isoenzymes and of high pl isoenzymes only were
     highly pos. correlated with amylase enzyme activity and neg. correlated
     with FN. The correlations were similar for detection of both isoenzyme families and for detection of high pI isoenzymes only. Analyses of three
     sets of wheat samples from different environments demonstrated that the
     relationship between ELISA absorbance and FN had little dependence on
     wheat cultivar. The precision of sample anal. using the field ELISA was
```

similar to the precision of FN test app.

9000-90-2, .alpha.-Amylase

NGUYEN 09/830,876

RL: ANT (Analyte); ANST (Analytical study)
(field ELISA for detection of .alpha.-amylase in
preharvest-sprouted wheat)
REFERENCE COUNT: 45 THERE ARE 45 CITED REFEREN

THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d ibib abs 19 1-51

ANSWER 1 OF 51' CAPLUS COPYRIGHT 2003 ACS on STN

2002:397370 CAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 138:38254

Simple ELISA Detection of a New Polymorphic Ha Locus TITLE:

Encoded Protein

AUTHOR(S): Partridge, M. A. K.; Appels, R.; Skerritt, J.

CORPORATE SOURCE: CSIRO Plant Industry and Quality Wheat CRC Ltd,

Canberra, 2601, Australia Journal of Cereal Science (2002), 35(2), 189-200 SOURCE:

CODEN: JCSCDA; ISSN: 0733-5210

Elsevier Science Ltd. PUBLISHER:

Journal DOCUMENT TYPE: LANGUAGE: English

A rapid two-site sandwich ELISA was developed for detection of a previously uncharacterized protein encoded at the Ha locus on chromosome 5DS of wheat (Triticum aestivum). The assay used the combined specificity of two antibodies to detect a protein that was sol. in aq. alc. salt solns. and water. It was expressed in the endosperm of all soft wheats and Triticum tauschii accessions tested. The ELISA was highly specific, with no signal obtained with varieties that did not express the protein. The presence of the 5DS-encoded protein correlated with a significant change in both water absorption and av. hardness and particle size indexes in a doubled haploid population derived from a cross between cvs. Cranbrook.times.Halberd. Only some hard varieties expressed this protein indicating that the protein is not predictive for hardness. However, it may be a new factor, or a marker for a new factor, affecting kernel texture. A polypeptide of Mr 66 000 was purified from an ext. of Halberd flour by immunoaffinity chromatog. Its N-terminal amino acid sequence identified it as an albumin with high homol. to both mammalian serum albumins and sucrose synthase from a range of cereals. The assay may be valuable in wheat breeding programs for assessing kernel texture where the parents are of different ELISA phenotype, or for varietal identification, as the expression of the polypeptide is variable

in hard wheat varieties.

THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS

REFERENCE COUNT: 40

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 2 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN 2001:76313 ACCESSION NUMBER: CAPLUS

DOCUMENT NUMBER: 134:251498

A new candidate protein for high lysine content in TITLE:

wheat grain

Singh, Jaswinder; Sharp, Peter J.; Skerritt, John AUTHOR(S):

CSIRO Plant Industry and Quality Wheat CRC Ltd,

CORPORATE SOURCE:

Canberra, 2601, Australia

Journal of the Science of Food and Agriculture (2001), 81(2), 216-226 SOURCE:

CODEN: JSFAAE; ISSN: 0022-5142

John Wiley & Sons Ltd. PUBLISHER:

DOCUMENT TYPE: Journal LANGUAGE: English

Translation elongation factor 1.alpha. (EF-1.alpha.) from cereal embryo was recently reported to be rich in lysine, and the possibility of using this protein as a marker for feed quality was explored in maize. this study we used immunochem. methods to investigate the relationship between the content of EF-1.alpha. and other proteins from wheat germ and lysine content in both hexaploid (bread) wheats and diploid wheat progenitors to the wheat A-genome. The levels of grain lysine, as well as their variation between lines or cultivars, were greater for the diploid wheats. While there was a significant correlation between the levels of EF-1.alpha. and grain lysine content, the binding of antibodies to a protein of Mr 37000 showed a higher correlation. This protein was characterized by amino acid sequencing as fructose

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1,6-bisphosphate aldolase. The possibility of using fructose
     1,6-bisphosphate aldolase as a marker for feed quality and development of
     a simple ELISA for quantification of lysine in wheat is demonstrated.
                                THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
                          30
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
    ANSWER 3 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                          2000:161331 CAPLUS
DOCUMENT NUMBER:
                          132:206946
                          Discrimination of glutenin subunits of wheat
TITLE:
INVENTOR(S):
                          Giersch, Thomas Mario; Skerritt, John Howard
                          ; Hill, Amanda Susanne
PATENT ASSIGNEE(S):
                          Quality Wheat Crc Limited, Australia
SOURCE:
                          PCT Int. Appl., 58 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:
                          Patent
LANGUAGE:
                          English
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                      KIND
                            DATE
                                            APPLICATION NO.
     WO 2000012557
                             20000309
                                            WO 1999-AU690
                                                              19990827
                       Α1
         W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE
     AU 9956116
                                             AU 1999-56116
                            20000321
                                                              19990827
                        A1
PRIORITY APPLN. INFO.:
                                          AU 1998-5548
                                                           A 19980828
                                          WO 1999-AU690
                                                           W 19990827
     Antibodies and immunoassays are disclosed for discriminating
     different high mol. wt. glutenin subunits (HMW-GS) in wheat.
     antibodies and immunoassays allow for the identification of
     preferred cultivars in plant breeding and for detn. of HMW-GS in wheat
     grain sample such as meal, flour and wheat grain ext.
                                THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
                          5
                                RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 4 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                          1998:80631 CAPLUS
DOCUMENT NUMBER:
                          128:165067
TITLE:
                          Identification and characterization of U.S. wheats
                          carrying null alleles at the wx loci
                          Graybosch, R. A.; Peterson, C. J.; Hansen, L. E.;
AUTHOR(S):
                          Rahman, S.; Hill, A.; Skerritt, J. H.
CORPORATE SOURCE:
                          USDA-ARS, University of Nebraska, Lincoln, NE, 68583,
SOURCE:
                          Cereal Chemistry (1998), 75(1), 162-165
                          CODEN: CECHAF; ISSN: 0009-0352
                          American Association of Cereal Chemists
PUBLISHER:
DOCUMENT TYPE:
                          Journal
LANGUAGE:
                          English
     Granule-bound starch synthase (GBSS) is the primary enzyme responsible for
     the synthesis of amylose in amyloplasts of cereal endosperm
     cells. Bread wheats, due to their hexaploid genetic system, carry three
     genes (wx loci) encoding GBSS. Purifn. and sepn. of GBSS from more than
     200 North American hexaploid wheats allowed the indentification of
     genotypes that carry null alleles at either the wx-A1 and wx-B1 loci.
     addn., the cultivar Ike carried both wx-A1 and wx-B1 null alleles. No wx-D1 nulls were detected. Null alleles were found in 10% of the hard
     winter wheats tested, but in only 2% of the samples soft winter wheats.
     Amylose contents of wheats carrying single null alleles at either the
     wx-A1 or wx-B1 loci often were lower than those of wild type wheats, but
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greater redn. in amylose content was obsd. in Ike. Monoclonal antibodies were used to quantify water-extractable GBSS in both wild-type and null genotypes. Gene dosage compensation was evident, although GBSS content, as measured by ELISA, was significantly lower in Ike than in all other wheats. The indentification of null alleles in

adapted genotypes suggests the development of wheats with a wide range of amylose contents will be possible by simple genetic crossing and selection.

REFERENCE COUNT:

12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 5 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1997:703350 CAPLUS

DOCUMENT NUMBER:

127:356397

TITLE:

Measurement of beta-amylase in malting barley (Hordeum vulgare L.). I. Development of a quantitative ELISA

for beta-amylase

AUTHOR(S):

Evans, D. E.; MacLeod, L. C.; Eglinton, J. K.; Gibson,

C. E.; Zhang, X.; Wallace, W.; Skerritt, J. H.; Lance, R. C. M.

CORPORATE SOURCE:

Dep. Plant Sci., Univ. Adelaide, Glen Osmond, SA 5064,

Australia

SOURCE:

Journal of Cereal Science (1997), 26(2), 229-239

CODEN: JCSCDA; ISSN: 0733-5210

PUBLISHER: DOCUMENT TYPE: Academic Journal

LANGUAGE:

English A double antibody, sandwich ELISA (ELISA) was developed using

polyclonal **antibodies** specific to beta-amylase to est. the amt. of 'free' (sol. in aq. saline soln.) or 'combined' (extd. with saline soln, including reducing agent) beta-amylase protein in barley grain and malt. This ELISA was used to quantify the amt. of beta-amylase in barley grain and malt from four varieties grown at nine sites in South Australia in 1993. The antibody used to develop the ELISA reacted differently with beta-amylase dependent on whether the source was barley grain or malt, and on the

beta-amylase band pattern in isoelec. focussing (IEF) of the barley variety. On the basis of their IEF band patterns barley varieties were divided into two types, designated Bmy1-Sd1 and Bmy1-Sd2. Malting resulted in proteolytic cleavage of the beta-amylase peptide with a redn. in the apparent mol. wt. of up to Mr 4000 and the appearance of new malt beta-amylase IEF bands that were more basic. The new malt beta-amylase IEF band patterns still allowed the identification of the Bmy1-Sd1 and Bmy1-Sd2 IEF types despite the change in mol. wt. and pI. The data obtained using the beta-amylase ELISA were highly correlated with beta-amylase activity for both the free and combined fractions when the IEF band pattern and its source, barley grain or malt, were

taken into account.

ANSWER 6 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1996:324233 CAPLUS

DOCUMENT NUMBER:

125:8895

TITLE:

Rapid testing for insecticide residues in stored products using immuno- and enzyme- assays

AUTHOR(S):

Skerritt, J. H.; Hill, A. S.; Edward, S. L.; Beasley, H. L.; Lee, N.; McAdam, D. P.; Rigg, A. J.

CORPORATE SOURCE:

Division Plant Industry, CSIRO, Canberra, 2601,

Australia

SOURCE:

Stored Product Protection, Proceedings of the International Working Conference on Stored-Product Protection, 6th, Canberra, Aust., Apr. 17-23, 1994 (1994), Volume 2, 843-847. Editor(s): Highley, Ed. CAB International: Wallingford, UK.

CODEN: 62WJAN

Conference English

DOCUMENT TYPE:

Accurate knowledge of the presence and levels of protectant residues in stored products is important for several reasons: for adequate control of possible infestation, to ensure that levels do not exceed legal Maximum Residue Limits, and to police specifications in sale/export contracts. While residue levels can be accurately detd. by gas-chromatog., the large no. of samples and sampling times required for thorough monitoring led us

to develop an alternative method, suitable for on-site testing. Specific ${\bf antibodies}$ have been employed for the major ${\bf grain}$ protectants used in Australia and overseas: organophosphates (fenitrothion, chlorpyrifos-Me, pirimiphos-methyl), cabaryl, methoprene and synthetic pyrethroids (bioresmethrin, permethrin, phenothrin). Tests for deltamethrin and some other pyrethroids are under development. In addn., other grain protectant compds. such as malathion, methacrifos, dichlorvos, bromophos and etrimfos can be detected using a novel cholinesterase inhibition test. The reagents needed to perform the tests have been packaged into compact test kits, some of which are now com. available. All the immunoassay tests are performed in the same manner: grain or other commodity is extd. by blending in methanol, drops of the ext. added to an antibody-coated microwell or tube followed by drops of an enzyme conjugate soln. After a few minutes, the microwell or tube is washed in water to remove unbound components, then a color developer added. Different levels of protectant in the sample produce graded differences in yellow color. The cholinesterase test is performed similarly. Tests have been tuned for detection in the 0.05/0.1-10 ppm residue range in the commodity. Kits designed for simultaneous testing of a large no. of samples under lab. conditions have also been developed and are suitable for anal. of malted, baked or noodle end-products as well as raw grain. Insecticidal protectants are also important in developing countries. In a new collaboration with Indian scientists, we are extending this work to some other plant-based commodities and organochlorines, fungicides and other organophosphates. Advantages of immunoassay kits here will be the low capital and per-test costs.

ANSWER 7 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1996:172786 CAPLUS

DOCUMENT NUMBER:

124:255671

TITLE:

Cereal seed storage proteins

AUTHOR(S):

Skerritt, John H.; Tatham, Arthur S.

CORPORATE SOURCE: SOURCE:

Division Plant Industry, CSIRO, Canberra, Australia Structure of Antigens (1996), Volume 3, 349-86. Editor(s): Van Regenmortel, M. H. V. CRC: Boca Raton,

Fla.

CODEN: 57YWAS

DOCUMENT TYPE:

Conference; General Review

English LANGUAGE:

A review with approx. 225 refs. Topics discussed include prolamins, evolutionary relationships of prolamins, methods of anal. of prolamins as antigens, epitope mapping approaches, structure of gluten polymers, and structure in relation to celiac toxicity and allergenicity.

ANSWER 8 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1995:929212 CAPLUS

DOCUMENT NUMBER:

124:4892

TITLE:

The major proteins of wheat endosperm starch granules

AUTHOR(S):

Rahman, Sadequr; Kosar-Hashemi, Behjat; Samuel, Michael S.; Hill, Amanda; Abbott, David C.; Skerritt, John H.; Preiss, Jack; Appels, Rudi;

Morell, Matthew K.

CORPORATE SOURCE:

Cooperative Research Centre for Plant Science,

Canberra, 0200, Australia

SOURCE:

Australian Journal of Plant Physiology (1995), 22(5),

793-803

CODEN: AJPPCH; ISSN: 0310-7841

PUBLISHER:

Commonwealth Scientific and Industrial Research

Organization

DOCUMENT TYPE:

Journal English

LANGUAGE:

Wheat starch contains two classes of assocd. proteins: proteins which are embedded within the granule and loosely assocd. surface proteins. The characterization of the major proteins that are embedded in the granule are described. Gel electrophoresis on the basis of size resolved these proteins into five bands of mol. wts. 60, 75, 85, 100 and 105 kDa. These

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polypeptides were demonstrated to be within the granule by their resistance to proteinase K digestion when granules were ungelatinized. The N-terminal sequences of these polypeptides are reported. The most prominent polypeptide is the 60 kDa granule-bound starch synthase. N-terminal sequence obtained from the 75 kDa polypeptide shows homol. to rice sol. starch synthase. The 85 kDa band was resolved into at least two types of polypeptides, one of which reacted with polyclonal antiserum to the maize branching enzyme IIb. The 100 and 105 kDa polypeptides were located only in the granule and are related, on the basis of N-terminal sequence similarity and cross-reactivity to monoclonal antibodies SDS-PAGE and monoclonal antibody cross-reactivity expts. suggest that the 100 and 105 kDa polypeptides are absent from starch granules from all other species examd., including other cereals. Thus, all the major granule proteins are involved in starch biosynthesis.

ANSWER 9 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1995:58091 CAPLUS

DOCUMENT NUMBER:

122:8232

TITLE:

Applications and limitations of immunochemical analysis of biopolymer quality in cereals

AUTHOR(S):

Skerritt, J. H.; Andrews, J. L.; Blundell,

CORPORATE SOURCE: SOURCE:

M.; Beasley, H. L.; Bekes, F. Div. Plant Ind., CSIRO, Canberra, 2601, Australia Food and Agricultural Immunology (1994), 6(2), 173-84

CODEN: FAIMEZ; ISSN: 0954-0105 Carfax

PUBLISHER: DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

English

A review with 37 refs. The mixing and baking properties of wheaten doughs are detd. largely by the content, compn. and interactions of the major groups of flour proteins, the disulfide-bonded glutenin subunits and monomeric gliadins. Prediction of dough and bread quality is currently based on medium-scale rheol. and baking tests, but the slow throughput of such tests limits their use both by millers and baking companies and in early-generation screening by plant breeders. Thus identification and quantification of sp. flour proteins by immunoassay has the potential advantages of speed, simplicity and applicability to small samples in breeding. Tech. problems can arise from the low solubilities of these proteins and their high degrees of sequence homol. (which often give rise to extensive antibody cross-reaction). These problems can be minimized by modifications to methods and combining monoclonal antibodies with selected extn. conditions to enhance the functional specificity of the assay. Limitations also arise from attempting to predict the behavior of a complex system, in which mol. interactions and processing changes have been important, purely from flour polypeptide compn. The authors have used quant. immunoassays for sp. groups of glutenins and gliadins to predict aspects of dough strength and extensibility, while 'yes-no' direct enzyme-linked immunosorbent assays can be used to screen for products of particular wheat or translocated rye genes assocd. with sp. dough qualities. Monoclonal antibodies are also being employed to purify sp. flour proteins under non-denaturing conditions and in conjunction with novel very small scale dough testing equipment to directly assess functionality in doughs.

ANSWER 10 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1995:34291 CAPLUS 122:104453

DOCUMENT NUMBER: TITLE:

Quality-related epitopes of high Mr subunits of wheat

alutenin

AUTHOR(S):

Andrews, J. L.; Skerritt, J. H.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Cereal Science (1994), 19(3), 219-29

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE:

Journal English

LANGUAGE: AB

Three hundred and eighty-four immobilized overlapping nonapeptides, corresponding to the full amino acid sequences of three high Mr subunits

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of glutenin from bread wheat (Triticum aestivum) grain, were used to det. the linear epitopes recognized by four monoclonal antibodies. These antibodies were selected on the basis of significant and pos. correlations between their binding to wheat flour exts. in a two-site (sandwich) enzyme immunoassay and rheol. measures of dough strength, an important aspect of bread wheat quality. The antibodies did not bind to a single, specific sequence but bound a series of related peptides in each high Mr glutenin subunit examd. The sequences recognized were not identical for the four antibodies, but in each case were in the central repeating domain of the high Mr glutenin subunits, and usually comprised regions that overlapped the degenerate repeat nonamer and hexamer sequences. High Mr glutenin subunits that have been assocd. with greater dough strength, such as the D-genome allelic products 1Dx5 and 1Dy10, displayed an increased no. of the epitope sequences. The location of the epitopes in sequences of overlapping .beta.-turns in the repetitive region supports the hypothesis that dough elasticity arises partly from .beta.-turn-forming secondary structure in the repeat regions of the Mr glutenin subunits. Addnl. .beta.-turns within high Mr subunits may extend their structure to allow increased interaction between the glutenin subunits and with the other proteins of the gluten complex, thus improving dough strength.

ANSWER 11 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268438 CAPLUS

DOCUMENT NUMBER: 120:268438

TITLE: Improved immunoassay for chlorpyrifos-methyl (Reldan)

in grain.

Edward, Simone L.; Skerritt, John H.; Hill, AUTHOR(S):

Amanda S.; McAdam, David P.

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Food and Agricultural Immunology (1993), 5(3), 129-44 CORPORATE SOURCE: SOURCE:

CODEN: FAIMEZ; ISSN: 0954-0105

DOCUMENT TYPE: Journal

LANGUAGE: English

An improved immunoassay for Reldan in grain was developed, based on an immobilized polyclonal antibody. This assay had greater sensitivity (limit of detection of 0.cntdot.02 ppm in grain, or O.cntdot.05-O.cntdot.1 ppb in buffer), was less susceptible to interference from methanol (used to ext. the residue from grain) and had greater precision than the earlier monoclonal antibody assay (Skerritt, J.H., et al, 1992). The polyclonal antibody exhibited greater cross-reaction with chlorpyrifos-Et (not used as a grain protectant), but less with fenchlorphos and bromophos (used occasionally as grain protectants), and employed a more stable peroxidase conjugate than the monoclonal antibody assay. Good correlations were obtained between Reldan residue levels in wheat grain detd. by the improved immunoassay and by gas chromatog. The properties of the polyclonal antibody should also allow its use in a rapid field assay.

ANSWER 12 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268419 CAPLUS

DOCUMENT NUMBER: 120:268419

TITLE: Rapid field tests for the organophosphorus pesticides,

fenitrothion and pirimiphos-methyl--reliable estimates

of residues in stored grain

Beasley, H. L.; Skerritt, J. H.; Hill, A. AUTHOR(S):

S.; Desmarchelier, J. M.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Stored Products Research (1993), 29(4), SOURCE:

357-69

CODEN: JSTPAR; ISSN: 0022-474X

DOCUMENT TYPE: Journal English LANGUAGE:

In order for grain handlers and traders to reliably est. residues of grain protectants in the field, antibody

-based tests were developed for the organophosphorus pesticides,

fenitrothion and pirimiphos-Me. To complement the rapid anal., rapid but efficient extn. techniques were developed. In these tests, a pesticide-contg. methanol ext. of the grain sample and an enzyme-labeled component are added dropwise to precoated tubes contg. buffer. After a brief incubation, the tubes are rinsed out in tap water and a substrate/chromogen for the enzyme is added. The color developed is stabilized by acidification and the test result read either by eye or in a portable field photometer. Significant levels of the particular pesticide result in a pale color compared to a dark green pesticide-free control. No calcns, were required to provide a quant, est, of residue as this could be read directly from a graph of color yield (absorbance) vs logarithm of pesticide concn., using std. solns. of pesticide. For fenitrothion, the test had a limit of detection of 4 ng/mL (0.1 ppm in grain) and gave quant. ests. in the range 0.5-15 ppm (in the grain), while the pirimiphos-Me test had a limit of detection of 1 ng/mL (0.03 ppm in grain) and gave quant. ests. over the range 0.1-15 ppm. Thus both tests can be used to segregate "pesticide-free" grain, with residues below 0.1 ppm. Data obtained using the field test correlated well with those obtained using lab. methods, including both gas-liq. chromatog. and immunoassay using microwell plates. The field immunoassay reagents were formatted into a small prototype test kit, and the components stabilized for field use.

ANSWER 13 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1994:268414 CAPLUS

DOCUMENT NUMBER:

120:268414

TITLE:

Analysis of the grain-protectant pesticides chlorpyrifos-methyl and methoprene with a 15-min

immunoassay for field or elevator use

AUTHOR(S):

Edward, Simone L.; Hill, Amanda S.; Ashworth, Paul;

Matt, Jonathan; Skerritt, John H.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, Australia Cereal Chemistry (1993), 70(6), 748-52

SOURCE:

CODEN: CECHAF; ISSN: 0009-0352

Journal English

DOCUMENT TYPE:

Antibody-based tests for field use have been developed to enable semiquant. anal. of two grain protectants, chlorpyrifos-Me and methoprene. In these tests, a pesticide-contg. methanol ext. of the

ANSWER 15 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1993:664564 CAPLUS

DOCUMENT NUMBER:

TITLE:

Quantitation of bioresmethrin, a synthetic pyrethroid

grain protectant, by enzyme immunoassay

AUTHOR(S):

Hill, Amanda S.; McAdam, David P.; Edward, Simone L.;

Skerritt, John H.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, NSW 2113, UK Journal of Agricultural and Food Chemistry (1993),

41(11), 2011-18

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE:

Journal

English

An enzyme immunoassay was developed for the synthetic pyrethroid, bioresmethrin, by use of a novel approach for synthesis of the pyrethroid-protein hapten conjugate for antibody prepn. Bioresmethrin was hydrolyzed at the ester linkage, and following protection-of-the-chrysanthemic-acid-group,-the-2-methylprop-1-ene substituent was oxidatively cleaved. The newly formed and unprotected acid group was reesterified to the other bioresmethrin hydrolysis product [[2-(phenylmethyl)-4-furyl]-methanol], and following substitution of the protecting group, the hapten was coupled to either protein for antibody prodn. or peroxidase for use in the immunoassay. The most sensitive assay employed an antibody prepd. to a deriv. with a 4-carbon spacer arm between bioresmethrin and carrier protein, but used a bioresmethrin-enzyme reporter prepd. using a 4-

(aminomethyl)cyclohexane-carboxylic acid spacer arm (limit of detection 2 ppb in buffer, 50 ppb in whole wheat or barley grain). Good correlations between HPLC and ELISA detns. of bioresmethrin in whole or ground barley grain were obtained. The sensitivity of the assay was slightly lower in ground grain or flour milling fractions due to interference from coextractives in methanol exts. Apart from resmethrin, of which bioresmethrin is the 1R,3R-trans-isomer, the assay did not detect a variety of other pyrethroids in com. use.

ANSWER 16 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1993:537750 CAPLUS

DOCUMENT NUMBER:

119:137750

TITLE:

A simple antibody-based test for dough strength. III. Further simplification and

collaborative evaluation for wheat quality screening Andrews, John L.; Blundell, Malcolm J.; Skerritt,

John H.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Cereal Chemistry (1993), 70(3), 241-6

SOURCE:

AUTHOR(S):

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE:

Journal

LANGUAGE:

English

An antibody-based method for discrimination of wheat flours or whole meals on the basis of differences in dough strength (Skerritt 1991b), as measured by extensigraph max. resistance for example, was simplified for use in large-scale screening to predict dough quality. major modification was the addn. of unlabeled antibody to the dild. grain ext. being analyzed, which simplified sample handling. It reduced the dilm. of the grain exts, being tested and improved the differentiation between flours of different strengths. method was also developed for simultaneous extn. and testing of sets of 96 unweighed whole meal samples. The method was tested in a collaboration trial in eight labs. (none with significant prior immunoassay experience) using two sep. analyses of a set of 16 flours, including three blind duplicates. Each lab. reported highly significant correlations between color developed in the assay and rheol. measurements of dough strength, such as farinograph development time and extensigraph max. resistance. Good ests. of within- and between-lab. precision were also obtained, indicating that the method was suitable for quality assessment in wheat breeding.

ANSWER 17 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1992:488842 CAPLUS

DOCUMENT NUMBER:

117:88842

TITLE:

Mono- and polyclonal antibodies to the

organophosphate fenitrothion. 1. Approaches to

hapten-protein conjugation

AUTHOR(S):

McAdam, David P.; Hill, Amanda S.; Beasley, Helen L.;

Skerritt, John H.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, Canberra, 2601, Australia

SOURCE:

Journal of Agricultural and Food Chemistry (1992),

40(8), 1466-70 CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Three different chem. approaches were used to couple the organophosphorus pesticide fenitrothion to carrier proteins for prodn. of polyclonal and monoclonal antibodies. Hapten conjugates coupled through the pesticide phosphate group yielded the most specific and highest affinity antibodies, although antibodies of moderate affinity were obtained by derivatization and coupling through the arom. nitro group following its redn. and amide formation with an adipic acid spacer arm. Assay formats using either immobilized antibody or immobilized hapten-protein conjugate could be used to det. free fenitrothion. The most sensitive assay could detect 1 ng of fenitrothion. It is recommended for the detection of residues of fenitrothion used for the protection of stored cereals.

ANSWER 18 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

117:88841

ACCESSION NUMBER: DOCUMENT NUMBER:

1992:488841 CAPLUS

TITLE:

Mono- and polyclonal antibodies to the organophosphate fenitrothion. 2. Antibody

specificity and assay performance

AUTHOR(S):

Hill, Amanda S.; Beasley, Helen L.; McAdam, David P.;

Skerritt, John H.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Agricultural and Food Chemistry (1992),

40(8), 1471-4

CODEN: JAFCAU; ISSN: 0021-8561

Journal English

DOCUMENT TYPE: LANGUAGE:

The performance and specificities of antibody-based assays for fenitrothion (I) were studied. I could be detected in grain in assays with either polyclonal or monoclonal antibodies using either immobilized antibody or immobilized hapten-protein conjugates. Most assay formats and antibodies distinguished I from structurally similar organophosphates, and variable extents of cross-reaction with metabolites were obsd. The concn. of I in wheat grain samples was measured in 3 assay formats with 2 antibodies, and in each case good correlations were obtained with
the results obtained by gas-liq. chromatog. For routine use, a format detecting 3 ng and suitable for anal. over the range 100 ppb-20 ppm in grain was preferred.

ANSWER 19 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1992:446860 CAPLUS

DOCUMENT NUMBER:

117:46860

TITLE:

Enzyme-linked immunosorbent assay for quantitation of organophosphate pesticides: fenitrothion,

chlorpyrifos-methyl, and pirimiphos-methyl in wheat

grain and flour-milling fractions

AUTHOR(S):

Skerritt, John H.; Hill, Amanda S.; Beasley,

CORPORATE SOURCE: SOURCE:

Helen L.; Edward, Simone L.; McAdam, David P. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of AOAC International (1992), 75(3), 519-28

CODEN: JAINEE; ISSN: 1060-3271

DOCUMENT TYPE:

Journal English

LANGUAGE:

Simple, competitive enzyme-linked immunosorbent assays (ELISAs) were developed for the quantitation of each of 3 major organophosphate insecticides: fenitrothion (FN), chlorpyrifos-Me (CPM), and pirimiphos-Me (PIRM). The performance of these assays on wheat **grain** and (for FN and CPM) on milling fractions such as flour, wheat germ, and bran was assessed. Each assay was specific for the particular compd., i.e., no significant cross-reaction with the other 2 pesticides was obsd. limited reactions were noted with major metabolites or analogs of these pesticides. Assay limits of detection of 0.3 ng FN, 0.2 ng CPM, and 0.02 ng PIRM were recorded, corresponding to limits of detection in whole grain of 0.08 ppm FN, 0.2 ppm CPM, and 0.03 ppm PIRM. Each compd. in grain and milling fractions could be extd. quant. by shaking in MeOH. Multiresidue anal. of the 3 insecticides was performed by simultaneously adding the cereal ext. (dild. in phosphate buffer) to sep. duplicate microwells coated with antibodies to FN, CPM, and PIRM and adding appropriate pesticide-horseradish peroxidase conjugates. High correlations between gas chromatog. and the ELISA methods were obtained for insecticide levels in whole wheat and in milling fractions. The ELISA assays had precision similar to those of instrumental pesticide analyses.

ANSWER 20 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1992:446838 CAPLUS

DOCUMENT NUMBER:

117:46838

TITLE:

Analysis of the synthetic pyrethroids, permethrin and

NGUYEN 09/830,876

1(R)-phenothrin, in grain using a monoclonal antibody-based test

AUTHOR(S):

CORPORATE SOURCE: SOURCE:

Skerritt, John H.; Hill, Amanda S.; McAdam, David P.; Stanker, Larry H. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Agricultural and Food Chemistry (1992),

40(7), 1287-92 CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE:

Journal

English LANGUAGE: A monoclonal antibody generated to the synthetic pyrethroid-related hapten, (3-phenoxybenzyl)-2,2-dimethylcyclopropane-1,3dicarboxylate-protein conjugate, was used to develop assays for detg. permethrin and 1(R)-phenothrin in wheat grain and flour milling fractions. The earlier 3-h assay was simplified by using 2 approaches. The antibody was directly conjugated to the enzyme horseradish peroxidase (HRP), which eliminated a sep. incubation and washing step from the assay. Also, an assay was developed with microwell-bound monoclonal antibody and a HRP-labeled 3-phenoxybenzoic acid deriv. These assay formats have advantages in increased sensitivity and, in the case of the latter assay, accuracy with grain and flour samples. The most sensitive assay format could detect 1.5 ng/mL permethrin; 50% inhibition of antibody binding occurred at 10 ng/mL. These values corresponded to 75 ppb and 500 ppb, resp., in the original wheat sample. MeOH was the most effective pyrethroid extractant. Use of a simple cleanup procedure for ground grain exts. improved ELISA

ANSWER 21 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1992:127228 CAPLUS

DOCUMENT NUMBER:

116:127228

accuracy but could be omitted for screening purposes.

TITLE:

Cellular and humoral responses in celiac disease. 2.

Protein extracts from different cereals

AUTHOR(S):

Skerritt, John H.; Devery, Jannine M.;

CORPORATE SOURCE:

Penttila, Imme A.; LaBrooy, Justin T. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Clinica Chimica Acta (1991), 204(1-3), 109-22

SOURCE:

CODEN: CCATAR; ISSN: 0009-8981

DOCUMENT TYPE:

Journal

LANGUAGE:

English

The humoral and cellular immune responses to grain protein exts. from celiac-toxic and non-toxic cereals were compared by use of a no. of ELISA and immunoblotting methods and the indirect leukocyte migration inhibition factor (LMIF) assay. Both adult and child celiacs had elevated levels of serum antibody to proteins from the celiac-toxic cereals, namely bread wheat, durum wheat, rye and barley and low levels of proteins from other cereals. Using protein-blotting techniques, antibody binding was greatest to gliadins/low-mol.-mass glutenin subunits and homologous prolamins from rye and barley, consistent with the ELISA findings. Competition ELISA and preabsorption tests indicated that antibody reaction to maize storage proteins did not simply result from cross-reaction of antigliadin antibodies. In LMIF assays, only the wheat exts. had activity in celiac patients. This is most likely partly due to loss of some T-cell epitopes from the extn. technique required for these proteins, as well as the relatively small effects seen for even very active fractions in the LMIF assay.

ANSWER 22 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1992:55602 CAPLUS

DOCUMENT NUMBER:

116:55602

TITLE:

Immunocytochemical localization of wheat storage proteins in endosperm cells 30 days after anthesis

AUTHOR(S):

Stenram, Unna; Heneen, Waheeb K.; Skerritt, John

CORPORATE SOURCE:

Dep. Crop Genet. Breed., Swed. Univ. Agric. Sci.,

Svaloev, S-268 00, Swed.

SOURCE:

Journal of Experimental Botany (1991), 42(244),

CODEN: JEBOA6; ISSN: 0022-0957

DOCUMENT TYPE:

Journal

LANGUAGE: English

Antisera against seven different wheat (Triticum aestivum) storage protein subfractions were characterized using (1) ELISA with gliadins and low- and high-mol. wt. glutenin subunits and (2) electrophoresis (SDS-PAGE and acidic buffer PACE) and immunoblotting. The specificities of these antisera (polyclonal antibodies) and 13 monoclonal antibodies covered various patterns of reactivity with alphabeta-, gamma- and omega-gliadins and low- and high-mol. wt. glutenins. The antisera and antibodies were applied to ultrathin sections of wheat endosperm tissue, from kernels fixed 30 days after anthesis, and were detected by secondary **antibodies** tagged with either 5 or 15 nm gold particles using transmission electron microscopy. Labeling was denser when the small gold particles were used but irresp. of gold particle size, labeling of polyclonal antisera predominated when the endosperm cells were subjected to both mono- and polyclonal antibodies. Each of the antisera and monoclonal antibodies that labeled the protein bodies, labeled them more or This indicates that only one kind of protein body, contg. less uniformly. all gliadin and glutenin subfractions, exists during this stage of grain development. Electron-dense globular inclusions found in many protein bodies were not labeled. Label was also found on protein-like material present in the lumen of the rough endoplasmic reticulum and on vesicles of the Golgi app. Thus, concn. of storage proteins takes place both at the site of synthesis, the lumen of the rough endoplasmic reticulum, and at the site of processing and transport, the vesicles of the Golgi app. Fusions between these proteinaceous materials give rise to larger protein bodies and ultimately to the protein matrix.

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ANSWER 23 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
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ACCESSION NUMBER: DOCUMENT NUMBER:

1991:605926 CAPLUS 115:205926

TITLE:

SOURCE:

Monoclonal and polyclonal antibodies and

test method for determination of fenitrothion and

closely related organophosphates

INVENTOR(S):

Skerritt, John Howard; Hill, Amanda Susanne;

McAdam, David Peter

PATENT ASSIGNEE(S):

Commonwealth Scientific and Industrial Research

Organization, Australia PCT Int. Appl., 30 pp.

CODEN: PIXXD2

DOCUMENT TYPE: LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 0100304		10010110	WO 1990-AU278	19900629
W: AU, CA,			WU 1990-AU278	19900629
			R, GB, IT, LU, NL, SE	
			CA 1990-2062820	
CA 2062820	C	20021112		
			AU 1990-58550	19900629
AU 633113				
			-ZA 1990=5132	
			EP 1990-909585	19900629
EP 479834	B1	19991110		
R: AT, BE,	CH, DE		R, GB, IT, LI, LU, NL	
JP 04503760 ·			JP 1990-509255	19900629
JP 08008874				
	_		AT 1990-909585	
		19960730	US 1994-300931	
PRIORITY APPLN. INFO	.:		AU 1989-5018 A	19890630

WO 1990-AU278 A 19900629 US 1991-784389 B1 19911230

OTHER SOURCE(S): MARPAT 115:205926

Monoclonal and polyclonal antibodies and fragments thereof are described which are capable of binding to specific members or groups of 0,0-dialkyl-O-(X) phosphorothioate compds. [X = (substituted) arom. or (substituted) heterocyclic group]. Hybridoma cell lines, methods for making antibodies and immunogens, and assays and kits including the antibodies are also disclosed. Thus, fenitrothian was converted to the diazonium salt and then conjugated with ovalbumin for prodn. of antibodies. The antibodies were used in a competitive enzyme immunoassay for fenitrothion in wheat.

ANSWER 24 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1991:603551 CAPLUS

DOCUMENT NUMBER:

115:203551

TITLE:

SOURCE:

Chromosomal control of wheat gliadin protein epitopes:

analysis with specific monoclonal antibodies

AUTHOR(S):

Skerritt, J. H.; Martinuzzi, O.; Metakovskii, E. V.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Theoretical and Applied Genetics (1991), 82(1), 44-53

CODEN: THAGA6; ISSN: 0040-5752

DOCUMENT TYPE:

Journal LANGUAGE: Enalish

The genetic relationships between small clusters of monomeric alc.-sol. wheat (Triticum aestivum L.) grain storage proteins (gliadins) were studied using a panel of monoclonal antibodies and immunoblotting, ELISA, and RIA methods. Use of Chinese Spring nullisomic-tetrasomic lines showed that several narrow-specificity antibodies bound specifically to gliadins encoded by genes located on a single chromosome. In at least one case, antibodies bound to genetic blocks of gliadins, indicating that these block members have structural homol. However, often not all gliadins of a block were recognized by an antibody. For broad-specificity antibodies and some narrow-specificity antibodies structural genes on several chromosomes were important. Studies with several primitive wheat species indicated that, while antibodies usually bound gliadins from the same genome in bread and primitive wheats, antibodies sometimes bound proteins of quite differing mobilities in the two wheat types. Use of antibodies to identify gliadin blocks is simpler than block anal. based on performing crosses, and should be of value in monitoring genotype/end-use quality relationships.

ANSWER 25 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN SSION NUMBER: 1991:581642 CAPLUS

ACCESSION NUMBER:

DOCUMENT NUMBER:

115:181642

TITLE:

Determination of the insect growth regulator

methoprene in wheat grain and milling fractions using an enzyme immunoassay

AUTHOR(S):

Hill, Amanda S.; Mei, Joanne V.; Yin, Chih Ming;

Ferguson, Bruce S.; Skerritt, John H. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

CORPORATE SOURCE: SOURCE:

Journal of Agricultural and Food Chemistry (1991),

39(10), 1882-6 CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE:

Journal LANGUAGE: English

The enzyme immunoassay of J. V. Mei, et al. (1990) was improved for the insect growth regulator methoprene, and the assay was used to det. methoprene in whole wheat grain and milling fractions, including flours, whole meal, bran, and wheat germ. Either MeOH or MeCN could be used to ext. methoprene from grain, flours, and bran; no cleanup of exts. was required. MeOH produced less matrix effects and could be tolerated at higher concns. in the assay. MeCN gave more reliable results in the extn. of methoprene from wheat germ. The improved assay had a sensitivity of 250 pg/mL, and 50% inhibition of antibody binding

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occurred at 3 ng/mL, corresponding to a max. sensitivity of 60 ppb and 50% inhibition of antibody binding at 0.75 ppm in the wheat sample when the routine assay method was used. The latter value is in keeping with residue levels typically found in methoprene-treated stored grain. Good correlations were found between methoprene detd. in wheat and grain fractions by the enzyme immunoassay and by conventional HPLC anal.

ANSWER 26 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN L9

ACCESSION NUMBER:

1991:557244 CAPLUS

DOCUMENT NUMBER:

115:157244

TITLE:

Testing cereal products and samples by

immunoassay. Test for organophosphate, carbamate, and

pyrethroid grain protectants

AUTHOR(S):

Skerritt, John H.; Robson, Lisa G.; McAdam,

David P.; Hill, Amanda S.

CORPORATE SOURCE:

Div. Plant Ind., Commonw. Sci. and Ind. Res. Organ., North Ryde, 2113, Australia

SOURCE:

ACS Symposium Series (1990), 451(Immunoassays Trace

Chem. Anal.), 124-38

CODEN: ACSMC8; ISSN: 0097-6156

DOCUMENT TYPE:

Journal

LANGUAGE: English

Organophosphates, synthetic pyrethroids and/or carbaryl are applied to stored grain and grain storage facilities to minimize insect infestation. Local industry deregulation coupled with increasingly stringent export residue tolerances and consumer demand for chem.-free foods have markedly increased demand for pesticide residue testing. Monoclonal and polyclonal antibodies have been prepd. and test methods developed for fenitrothion, the major organophosphate pesticide used on grain. Some antibodies were specific for fenitrothion and sensitive to 0.1-0.5 ng; other antibodies bound to closely related organophosphates as well. A simple cholinesterase inhibition test for general screening for organophosphates and carbamates is being adapted for use in field situations or high-throughput labs. Antibodies to certain pyrethroids (phenothrin, permethrin) are being assessed for use in simple test kits.

ANSWER 27 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1991:534290 CAPLUS

DOCUMENT NUMBER:

115:134290

TITLE:

Determination of gluten in foods using a monoclonal

antibody-based competition enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; Skerritt, John H.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Food and Agricultural Immunology (1990), 2(1), 21-35

SOURCE: CODEN: FAIMEZ; ISSN: 0954-0105

DOCUMENT TYPE:

Journal

LANGUAGE:

English

A sensitive competition enzyme-immunoassay for quantification of gluten in foods was developed, using horseradish peroxidase-labeled monoclonal antibodies. Selected antibodies specific for wheat .omega.-gliadin components were used, and these antibodies bound proteins from the related cereals, rye and barley, which are also toxic to individuals with gluten-intolerance (coeliac disease). Binding of these antibodies was not inhibited by heating of gluten during cooking or baking and the assay did not detect cereals not toxic in coeliac disease, such as maize or rice.
Gluten could be quantified at higher levels in meat products or in cereal products such as flours or baked goods. Results were not affected by wheat variety. Quant. results could be obtained using simple extn. techniques and solvents (40% or 70% ethanol). Detection of gluten was quant. in a wide range of foods, except for certain products contg. gluten proteins that had been subjected to severe heat, enzymic, or chem. treatment. In these products overestimates rather than underestimates were usually obtained.

ANSWER 28 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

115:69981

ACCESSION NUMBER: DOCUMENT NUMBER:

1991:469981 CAPLUS

TITLE:

Immunology invades chemistry: testing cereals

with antibodies

AUTHOR(S):

Skerritt, John H.; Hill, Amanda S.; McAdam,

David P.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

Chemistry in Australia (1990), 57(9), 297-300

CODEN: CHAUDY; ISSN: 0312-8180

DOCUMENT TYPE:

Journal; General Review

LANGUAGE: Enalish

A review with 11 refs. of immunochem. assays used in cereal prodn. and processing, including detection of toxic, illegal, or quality component evaluating wheat gluten strength, dough extensibility, grain hardness, flour protein content and lipid and starch compn. variety identification, detection of pesticide residues, detection and detn. of gluten in foods, and detection of chill-proofing enzymes in beer.

ANSWER 29 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1991:183936 CAPLUS

DOCUMENT NUMBER:

114:183936

TITLE:

Enzyme immunoassay for determination of gluten in

foods: collaborative study

AUTHOR(S):

Skerritt, John H.; Hill, Amanda S.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal - Association of Official Analytical Chemists

(1991), 74(2), 257-64

CODEN: JANCA2; ISSN: 0004-5756

DOCUMENT TYPE: LANGUAGE:

Journal English

A collaborative study was performed in 15 labs. to validate a monoclonal antibody-based enzyme immunoassay (EIA) for detn. of gluten in foods. The study included 13 samples: corn starch, gluten-free baking mixes, wheat flours, cookies, cooked meats, and a soup. Gluten was present in these samples at either zero or 0.02 to 10% by wt., i.e., over almost 3 orders of magnitude. The mean assay values for the foods varied from 88 to 105% of the actual amts. The assay was quant. for cereal products and the soup with repeatability (RSDr, relative std. deviation) and reproducibility (RSDR) of 16-22% and 24-33%, resp.
The assay was semiquant. for the processed meat products (RSDr 14 and 26% and RSDR 46 and 56%), probably because gluten was unevenly distributed in the small (1 g) samples that were analyzed. The ELISA method produced no false pos. results, and false negatives obtained with tannin-contg. foods could be avoided by use of a modified sample extractant. None of the collaborators reported problems in following the protocol. The method has been adopted official first action by AOAC for detn. of wheat gluten in

ANSWER 30 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1991:78626 CAPLUS

DOCUMENT NUMBER:

114:78626

TITLE:

Immunological homologies between wheat gluten and

starch granule proteins

AUTHOR(S):

Skerritt, J. H.; Frend, A. J.; Robson, L. G.; Greenwell, P.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Cereal Science (1990), 12(2), 123-36

CODEN: JCSCDA; ISSN: 0733-5210

SOURCE:

Journal English

DOCUMENT TYPE: LANGUAGE:

Structural homologies between wheat (Triticum aestivum) gluten proteins and proteins present in well-washed starch granules were examd. with a panel of mouse monoclonal and mouse and rabbit polyclonal antibodies, using immunoblotting, ELISA, and immunocytochem. methods. Many antibodies raised against gluten protein fractions cross-reacted with starch granule proteins (SGP), but often

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weakly. Antibodies with similar gliadin and glutenin subunit specificities had similar SGP specificities. Antibodies to high-mobility (.alpha.-, .beta.-, .gamma.-) gliadins cross-reacted weakly with low-mol.-wt. SGP (Mr 8000, 19,000 and 30,000) on immunoblots, and very weakly in indirect ELISAs. Some of these antibodies labeled both protein bodies and the periphery of starch granules in sections of immature grain, consistent with low-mol.-wt. SGP deemed to be surface SGP on the basis of extractability studies, indeed being present on the granule surface. Monoclonal antibodies that bound .gamma.- or .omega.-gliadins and glutenin subunits bound to higher mol. wt. SGP, esp. a protein of Mr 77,000, at concns. only slightly above those which labeled gluten proteins. As the interior of the starch granule section was labeled, these proteins are likely to be integral to the granule. Antibodies binding broadly to all major gluten protein classes also bound most high and low-mol.-wt. SGPs. Some starch proteins of Mr 15,000, which have been assocd. with endosperm softness, appeared to be immunol, distinct.

ANSWER 31 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1990:629824 CAPLUS

DOCUMENT NUMBER:

113:229824

TITLE:

Wheat low-molecular-weight glutenin subunits structural relationship to other gluten proteins

analyzed using specific antibodies Skerritt, John H.; Robson, Lisa G.

AUTHOR(S): CORPORATE SOURCE:

Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde,

2113, Australia

SOURCE:

Cereal Chemistry (1990), 67(3), 250-7 CODEN: CECHAF; ISSN: 0009-0352

Journal English

DOCUMENT TYPE: LANGUAGE:

The immunol. homol. of low-mol. wt. glutenin subunits (LMW-GS) were compared with the other major wheat gluten polypeptides, high-mol.-wt. glutenin subunits (HMW-GS), and gliadins. Conventional 1-dimensional polyacrylamide gel electrophoretic (PAGE) methods were used as well as a 2-step, 1-dimensional sodium dodecyl sulfate-page technique, together with immunoblotting and enzyme-immunoassay methods. Many antibodies raised to gliadins and HMW-GS bound well to LMW-GS. Antibodies with specificities for similar groups of gliadins bound to similar groups of glutenins; and HMW-GS but not to other grain proteins, suggesting the existence of "common gluten" amino acid sequences or conformations. The soly. and immunochem. similarities as well as the known linkage between the genes for LMW-GS and certain gliadins mean that

LMW-GS may be responsible for many biochem. properties and quality effects usually attributed to gliadins.

ANSWER 32 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1990:512017 **CAPLUS**

DOCUMENT NUMBER:

113:112017

TITLE:

Cereal identification using

antibodies to characteristic protein, and kits

containing the antibodies

INVENTOR(S):

Skerritt, John Howawrd; Wrigley, Colin Walter; Underwood, Patricia Anne

PATENT ASSIGNEE(S):

Commonwealth Scientific and Industrial Research

Organization, Australia

SOURCE:

Pat. Specif. (Aust.), 12 pp.

CODEN: ALXXAP

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 592987	B2	19900201	AU 1986-57023	19850502
AU 8657023	A1	19861106		

PRIORITY APPLN. INFO.: AU 1985-401 19850502 A cereal variety or quality type is identified by applying a cereal grain ext. or grain germination product to a suitable support, treating the support with a (monoclonal) antibody to a specific protein, and detg. the amt. of bound antibody. In an EIA for barley using antibodies to Band C-hordeins, varieties more suitable for beer malting showed greater rates of destruction of antibody binding sites than poorer quality varieties. Assays using immobilized capture antibodies are also described.

ANSWER 33 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

1990:404802 CAPLUS

113:4802

TITLE:

Homologies between grain storage proteins of different cereal species. 2. Effects of assay format and grain extractant on

antibody cross-reactivity

AUTHOR(S):

CORPORATE SOURCE: SOURCE:

Skerritt, John H.; Hill, Amanda S. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Cereal Science (1990), 11(2), 123-41

CODEN: JCSCDA; ISSN: 0733-5210 Journal

DOCUMENT TYPE:

LANGUAGE: English

A variety of monoclonal antibodies with specificities for different wheat grain storage proteins has been shown to exhibit a no. of differing cross-reaction patterns with grain storage proteins from related cereal species (Skerett and Lew, 1990). This antibody library provides an opportunity to measure the effects of a range of immunoassay methodol. variables on the cross-reactivity of these antibodies. Variation of the extractant used for grain proteins from different cereals altered both the amt. and compn. of protein extd. and thus the cross-reaction of the antibodies. Antibody cross-reactivity was greater when nitrocellulose membrane solid phases compared with polystyrene microwells were used for indirect ELISA. Quite differing cross-reactivity results were obtained when the same grain protein exts. were used in indirect, antigen-competition and sandwich-type assay formats. In the sandwich assay format, alteration of either the solid phase-bound or labeled antibody altered apparent antibody specificity. Thus, it is important when reporting immunol. homol. data, to define cross-reaction of antibodies with respect to the assay format used. Antibody specificity (or cross-reactivity) can be manipulated by variation of sample extractant, solid phase and the format of the assay.

ANSWER 34 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1990:404801 CAPLUS

DOCUMENT NUMBER:

113:4801

TITLE:

Homologies between grain storage proteins of

different cereal species. 1. Monoclonal antibody reaction with total protein extracts

AUTHOR(S): CORPORATE SOURCE:

SOURCE:

Skerritt, John H.; Lew, Patricia Y. Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Cereal Science (1990), 11(2), 103-21

CODEN: JCSCDA; ISSN: 0733-5210 Journal

DOCUMENT TYPE:

English

LANGUAGE:

The interactions of a library of monoclonal antibodies, prepd. to wheat (Triticum aestivus L.) gluten proteins, with exts. of total seed storage protein from a no. of related cereals was studied qual. using SDS-PAGE and immunoblotting techniques and studied quant. using indirect enzyme-immunoassay. Antibodies were of four cross-reaction types: (1) some antibodies, such as many of those binding .alpha.- and .beta.-gliadins, bound selectively to wheat grain proteins, (2) others with similar gliadin specificities, bound to prolamins from other Festucoid species (rye, barley and oats),

(3) other antibodies specific for certain .gamma.- and omega.-gliadins and high-mol.-wt. glutenins, bound very well to proteins from wheat, rye and barley grain, while (4) some antibodies showed anomalous cross-reactivities, binding well to wheat and maize prolamins but very weakly to rye or barley grain proteins. These homologies were generally in keeping with structural homologies of proteins from various cereal grains obtained from DNA sequencing and cross-hybridization studies. In some cases, new homologies were identified.

ANSWER 35 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1990:156891 CAPLUS

DOCUMENT NUMBER:

112:156891

TITLE:

Antibody responses reveal differences in oral tolerance to wheat and maize grain

protein fractions

AUTHOR(S):

Johnson, R. B.; Labrooy, J. T.; Skerritt, J.

CORPORATE SOURCE: SOURCE:

Dep. Med., Univ. Adelaide, Adelaide, Australia Clinical and Experimental Immunology (1990), 79(1),

135-40

CODEN: CEXIAL; ISSN: 0009-9104

DOCUMENT TYPE:

Journal

LANGUAGE:

English The influence of diet on humoral immune responses to gluten- and corn-derived proteins was examd. by ELISA and protein blotting techniques. Mice raised on the corn-based (gluten-free) diet responded well to parenteral immunization with each of 6 gluten-derived protein prepns. (whole gliadin, 2 omega-gliadin fractions, wheat salt-sol. proteins, a peptic-tryptic digest, and a subtilisin digest of gluten); serum antibody levels increased at least 300-fold in each case. In contrast, mice raised on the wheat-based diet responded poorly to immunization with either whole gliadin or omega-gliadin and were virtually nonresponsive to enzymic digest of gluten. Diet had little effect on the magnitude of the **antibody** response to wheat salt-sol. proteins, with both groups showing a 300-fold increase in titer. Similarly tolerance to .alpha.-zeins, the alc.-sol. proteins of corn did not occur on either diet. Some oral tolerance was obsd. to corn glutelin. specificity of the various antibody responses was then analyzed by immunoblotting. Following immunization with gluten proteins or digests, antibodies from the corn-fed mice bound more or less equally to each of the main gliadin bands and to the glutenins, whereas the mice on the wheat-based diet had antibody specific for omega-gliadin proteins. Serum antibodies from the corn-fed mice, immunized with either .alpha.-zein or corn glutelin, showed even labeling of the major corn endosperm proteins whereas antibodies from mice on the wheat diet showed strong labeling of the mol. wt. 27,000 and 58,000 bands. Diet influenced the specificity, as well as the magnitude, of serum antibody responses to cereal proteins. In addn., oral tolerance appeared to affect the humoral response to some cereal proteins more than others. Both of these findings have important implications for the understanding of celiac disease.

ANSWER 36 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

1989:572723 CAPLUS 111:172723

TITLE:

SOURCE:

Detection of glutens with monoclonal antibody

-producing hybridoma cells

INVENTOR(S):

Skerritt, John Howard; Hill, Amanda Susanne Commonwealth Scientific and Industrial Research

PATENT ASSIGNEE(S):

Organization, UK Brit. UK Pat. Appl., 21 pp.

DOCUMENT TYPE:

CODEN: BAXXDU Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE		
			GB 1988-16366	19880708		
			AU 1988-18917	19880708		
CA 1294903	A1	19920128	CA 1988-571492	19880708		
AB Hybridoma cell line ATCC HB9798 producing monoclonal antibodies						
(Mabs) against .omegagliadin of wheat and related proteins in rye and						
barley is prepd. The Mabs can be used for quant. and qual. detn. of						
gluten in samples. Balb/c mice were grown on a gluten-free diet till						
parturition and mated. After weaning, the female progeny were reared for						
one month on the gluten-free diet and immunized with .omegagliadin.						
Spleens were removed from mice and the cells were fused with mouse myeloma						
cell line sp 2/0. After selection, hybridoma 401/21 subclones were						
screened and further grown as ascites tumors to obtain antibody						
401/21. The antibody 401/21 was immobilized on flat-bottom						
96-well polystyrene microwell plates or strips for ELISA of food samples.						
The method could detect 0.01 and 0.001% (wt./wt.) gluten in food samples						
depending upon the diln. of the gluten ext.: lower levels were detectable						
in more concd. e	xts.	•	*			
	GB 2207921 GB 2207921 AU 8818917 AU 611921 CA 1294903 ORITY APPLN. INFO. Hybridoma cell l (Mabs) against. barley is prepd. gluten in sample parturition and one month on the Spleens were rem cell line sp 2/0 screened and fur 401/21. The and 96-well polystyr The method could depending upon t	GB 2207921 A1 GB 2207921 B2 AU 8818917 A1 AU 611921 B2 CA 1294903 A1 ORITY APPLN. INFO.: Hybridoma cell line AT (Mabs) against .omega. barley is prepd. The gluten in samples. Ba parturition and mated. one month on the glute Spleens were removed f cell line sp 2/0. Aft screened and further g 401/21. The antibody 96-well polystyrene mi The method could detect	GB 2207921 A1 19890215 GB 2207921 B2 19910529 AU 8818917 A1 19890112 AU 611921 B2 19910627 CA 1294903 A1 19920128 ORITY APPLN. INFO.: Hybridoma cell line ATCC HB9798 prod (Mabs) against .omegagliadin of wl barley is prepd. The Mabs can be us gluten in samples. Balb/c mice were parturition and mated. After weanin one month on the gluten-free diet and Spleens were removed from mice and the cell line sp 2/0. After selection, screened and further grown as ascited 401/21. The antibody 401/21 was imm 96-well polystyrene microwell plates. The method cou'ld detect 0.01 and 0.01 depending upon the diln. of the gluteness.	GB 2207921 A1 19890215 GB 1988-16366 GB 2207921 B2 19910529 AU 8818917 A1 19890112 AU 1988-18917 AU 611921 B2 19910627 CA 1294903 A1 19920128 CA 1988-571492 ORITY APPLN. INFO.: AU 1987-2985 Hybridoma cell line ATCC HB9798 producing monoclonal a (Mabs) against .omegagliadin of wheat and related pr barley is prepd. The Mabs can be used for quant. and gluten in samples. Balb/c mice were grown on a gluten parturition and mated. After weaning, the female prog one month on the gluten-free diet and immunized with . Spleens were removed from mice and the cells were fuse cell line sp 2/0. After selection, hybridoma 401/21 s creened and further grown as ascites tumors to obtain 401/21. The antibody 401/21 was immobilized on flat-b96-well polystyrene microwell plates or strips for ELI The method could detect 0.01 and 0.001% (wt./wt.) glut depending upon the diln. of the gluten ext.: lower lev		

ANSWER 37 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1989:491681 CAPLUS

DOCUMENT NUMBER: TITLE:

111:91681 Monoclonal antibodies used to characterize

cDNA clones expressing specific wheat endosperm

proteins

AUTHOR(S):

Donovan, G. R.; Skerritt, J. H.; Castle, S.

CORPORATE SOURCE:

Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde,

Australia

SOURCE:

Journal of Cereal Science (1989), 9(2), 97-111

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE:

Journal

English LANGUAGE:

A wheat cDNA library, prepd. from grain endosperm poly A+ mRNA and cloned into the Escherichia coli expression vector lambda gt11, has been screened with 9 monoclonal antibodies having specificities for different wheat endosperm proteins. At least 1 pos. cDNA clone was isolated and purified from those selected with each antibody. Each purified cDNA clone was induced to express fusion proteins, and the nitrocellulose membranes to which the proteins were transferred were incubated with each of the other antibodies at .gtoreq.2 concns. to investigate the extent of homologies between expression fusion proteins. The specificities of the antibodies were detd. using immunoblotting under the same conditions used for binding to the fusion proteins from the expressed cDNA clones. Denatured DNA from each antibody-selected cDNA clone was also characterized by hybridization to .alpha.-/.beta.-genomic gliadin and genomic high-mol.-wt. glutenin subunit DNA probes. Northern hybridizations using the isolated cDNA as probes for endosperm mRNA were also used to assist clone identification. Some monoclonal antibodies with overlapping specificities (identified from blotting and ELISA expts.) crossreacted with several expressed cDNA clones. However, in other instances, pos. identifications were made of the proteins coded for by single families of the cDNA clones. Monoclonal **antibody** screening of a wheat cDNA library is useful in identifying families of cDNA clones corresponding to different wheat polypeptides at the primary screening stage, obviating the need in many instances for the application of more tedious methods of clone identification.

ANSWER 38 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN ACCESSION NUMBER: 1989:230112 CAPLUS

DOCUMENT NUMBER:

110:230112

TITLE:

Protein modification during malting and brewing: some

new analytical methods

AUTHOR(S):

Skerritt, J. H.; Collings, D.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, Australia

Proceedings of the Convention - Institute of Brewing (Asia Pacific Section) (1988), 20th, 87-93

CODEN: IBAZA2; ISSN: 0367-6897

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Modern protein anal. methods, including size-exclusion and reversed-phase HPLC, PAGE, and monoclonal antibody tests were used to examine protein modification in grain during malting and in mash exts. and wort in brewing. Size-exclusion HPLC and electrophoresis are useful for providing qual. anal. of malt modification and proteolysis and protein pptn. during mashing; hydrolysis of specific proteins can also be quantified by HPLC or by immunoassay. Other antibody tests to measure residual protein from malt and cereal adjuncts in finished beers and to det. whether proteolytic enzymes were used in chillproofing of beers are also described.

ANSWER 39 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1989:191088 CAPLUS

DOCUMENT NUMBER:

110:191088

TITLE:

Monoclonal antibody specific to gliadin

protein of wheat, its production and use in kits and

methods for detection of gliadin in food

INVENTOR(S):

Skerritt, John Howard; Wrigley, Colin Walter; Underwood, Patricia Anne

PATENT ASSIGNEE(S):

Commonwealth Scientific and Industrial Research

Organization, Australia Pat. Specif. (Aust.), 16 pp.

SOURCE:

CODEN: ALXXAP Patent

DOCUMENT TYPE: LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE AU 572955 19880519 AU 1985-38501 19840206

AU 8538501

19850815 **A1**

AU 1984-3475 19840206

PRIORITY APPLN. INFO.: A hybridoma is manufd. which produces antibody specific for heat-stable and low-mobility gliadin(s). The antibody is used in a kit and immunoassay method for detecting gliadin in food. Mice were immunized with purified bread wheat gliadin and the spleen cells were fused with mouse myeloma Sp2/O using PEG. The resultant hybrid cells were cloned and screened with wheat grain proteins. Of 386 clones examd., 2 secreted antibodies interacting with certain discrete bands in the .gamma.- and .omega.-gliadin regions of gradient gel electrophoresis-sepd. proteins. Neither rye pollen proteins nor a variety of other proteins (bovine milk .alpha.-lactalbumin, soybean trypsin inhibitor, etc.) bound these antibodies.

ANSWER 40 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1988:525977 CAPLUS

DOCUMENT_NUMBER:

109:125977

TITLE:

Accumulation of gliadin and glutenin polypeptides during development of normal and sulfur-deficient wheat seed: analysis using specific monoclonal

antibodies

AUTHOR(S):

Skerritt, J. H.; Lew, P. Y.; Castle, S. L.

CORPORATE SOURCE: SOURCE:

Div. Plant Ind., CSIRO, North Ryde, 2113, Australia Journal of Experimental Botany (1988), 39(203), 723-37

CODEN: JEBOA6; ISSN: 0022-0957

DOCUMENT TYPE:

Journal

Enalish I ANGUAGE: A panel of monoclonal antibodies with various specificities for wheat (Triticum aestivum) gluten polypeptides has been used to analyze the accumulation of these polypeptides in the endosperm of developing wheat seeds grown under normal and S-deficient conditions. Immunoblots of polypeptides fractionated by SDS-PAGE allowed a qual. anal. of gliadin and high-mol.-wt. (HMW) glutenin accumulation for high- and low-S seeds 8-30 days after anthesis (d.a.a.). In addn., quant. anal. of the deposition of various gluten polypeptides was performed, with a solid-phase RIA on exts. of seeds harvested 4-36 d.a.a. The initial accumulation of HMW glutenin subunits was detectable at an earlier stage of development than that of gliadins for both normal and S-deficient seeds. The initiation of detectable gliadin accumulation was asynchronous with an order of .alpha.-gliadins, .beta.-, .gamma.- and some .omega.-gliadins and finally the remaining .omega.-gliadins. In S deficiency, all gliadins reached a const. proportion of the dry wt. of the endosperm earlier than in normal wheat, while a more marked increase in the proportion of HMW glutenin occurred late in grain development. The protein blot studies also identified a putative .omega.-gliadin polypeptide which was detectable late in seed development and only in S-deficient seeds.

ANSWER 41 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1987:194871 CAPLUS

DOCUMENT NUMBER:

106:194871

TITLE:

Monoclonal antibodies in agricultural

testing: quantitation of specific wheat gliadins

AUTHOR(S):

affected by sulfur deficiency Skerritt, John H.; Martinuzzi, Ornella;

CORPORATE SOURCE: SOURCE:

ť.

Wrigley, Colin W. Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia Canadian Journal of Plant Science (1987), 67(1), 121-9

CODEN: CPLSAY; ISSN: 0008-4220

DOCUMENT TYPE:

Journal English

Proteins correlation with end-use quality in wheat (Triticum aestivum L.) flour samples have been quantitated using a panel of monoclonal. antibodies (MCA) with specificities for different gliadins (grain endosperm storage proteins which are sol. in aq. alc.). beta-gliadin specific antibody was found suitable for measuring sulfur-related quality loss in sets of flours from three wheat cultivars grown under varying conditions of sulfur fertilization. Binding of this monoclonal antibody, measured in a competitive enzyme-immunoassay, was highly correlated with flour sulfur and with the extensibility of, and resistance to stretching of doughs prepd. from these flour samples. These results demonstrate that monoclonal antibodies may be used to measure levels of specific components which vary as the technol. quality of the food varies. Rapid spot-tests based on the reaction of seed proteins with specific monoclonal antibodies may aid progeny selection in plant breeding program.

ANSWER 42 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1987:135178 CAPLUS

DOCUMENT NUMBER:

106:135178

TITLE:

Distinction between barley varieties by grain

characteristics, electrophoresis, chromatography and

antibody reaction

AUTHOR(S):

CORPORATE SOURCE: SOURCE:

Skerritt, J. H.; Wrigley, C. W.
Rohstoffábt., VLB, Berlin, D=1000/65, Fed. Rep. Ger.
Seed Science and Technology (1986), 14(3), 619-29

CODEN: SSTCBK; ISSN: 0251-0952

DOCUMENT TYPE:

immunol.

Journal; General Review English

LANGUAGE:

A review and discussion with 10 refs. of methods of identification of barley varieties, e.g., visual examn., gel electrophoresis, HPLC, and

NGUYEN 09/830,876

Improved staining and characterization of proteins

following gel electrophoresis and electroblotting Wrigley, Colin W.; Skerritt, John H. Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

ANSWER 43 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

1987:115996 106:115996

ACCESSION NUMBER:

DOCUMENT NUMBER:

TITLE:

AUTHOR(S): CORPORATE SOURCE: CAPLUS

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Electrophor. '86 [Eighty-Six], Proc. Meet. Int. Electrophor. Soc., 5th (1986), 291-303. Editor(s): Dunn, Michael J. VCH: Weinheim, Fed. Rep. Ger.
SOURCE:
                          CODEN: 55IZAB
                          Conference
DOCUMENT TYPE:
                          English
LANGUAGE:
     Improvements in immunol. techniques for characterizing protein zones after
     gel electrophoresis and electrophoretic transfer to nitrocellulose are
     illustrated, using wheat grain proteins as antigens and
     monoclonal or serum antibodies. Techniques included alkali
     enhancement of protein staining and immunol. reactivity of electroblotted
     proteins, avoidance of nonspecific antibody binding, and
     preparative use of electroblotting for protein purifn.
     ANSWER 44 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
                           1987:48365
                                       CAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                           106:48365
                           Specificity characteristics of monoclonal
TITLE:
                           antibodies to wheat grain storage
                           proteins
                           Skerritt, John H.; Underwood, P. Anne
AUTHOR(S):
                           Div. Mol. Biol., CSIRO, North Ryde, 2113, Australia
CORPORATE SOURCE:
                           Biochimica et Biophysica Acta (1986), 874(3), 245-54
SOURCE:
                           CODEN: BBACAQ; ISSN: 0006-3002
                           Journal
DOCUMENT TYPE:
                           English
LANGUAGE:
      A variety of monoclonal antibodies was prepd. to wheat (Triticum
      aestivum) gluten proteins, and their antigenic specificities were assessed
      using non-denaturing polyacrylamide gradient and SDS-PAGE and
      immunoblotting techniques. While most anti-gliadin monoclonal
      antibodies bound to all gliadin protein bands sepd. by
      1-dimensional electrophoresis, several antibodies binding to
      small groups of gliadin proteins were identified. At high concns., these
      specific antibodies bound to an increasing no. of gliadins; this
      is likely due to the very high sequence homologies between groups of
      gliadin proteins. Several monoclonal antibodies with specificities for glutenin proteins were produced. These
      antibodies bound to all major glutenin subunits, although at low
      antibody concns. some bound selectively to a single subunit.
      Other anti-glutenin antibodies bound to minor glutenin subunits
      and a variety of gliadin proteins. Several bound to .gamma.-gliadins and
      high-mol.-wt. glutenins, suggesting that these groups of proteins bear
      considerable homol. The results are reviewed in relation to known
      information on gluten protein structure, derived from DNA-sequencing
       studies.
      ANSWER 45 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
                            1986:624490 CAPLUS
 ACCESSION NUMBER:
                            105:224490
 DOCUMENT NUMBER:
                            New approaches to barley variety identification and
  TITLE:
                            quality studies
                            Skerritt, J. H.; Batey, I. L.; Wrigley, C.
 AUTHOR(S):
                            Wheat Res. Unit, CSIRO, North Ryde, Australia
  CORPORATE SOURCE:
                            Proceedings of the Convention - Institute of Brewing
  SOURCE:
                             (Asia Pacific Section) (1986), 19th, 55-62
                             CODEN: IBAZA2; ISSN: 0367-6897
  DOCUMENT TYPE:
                             Journal
                            English
  LANGUAGE:
       Three new approaches, which rely on differences in hordein compn. or
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properties, were investigated for their suitability as barley variety identification methods, to supplement visual and electrophoretic methods. High-performance liq. chromatog. on either ion-exchange or reversed-phase columns can differentiate barley varieties that cannot be distinguished by electrophoresis. Differences in the interaction of hordeins from various varieties with a set of monoclonal antibodies may form the basis for rapid spot-test for confirmation of variety or quality type. In addn., a very simple test based upon differences in the turbidity of grain exts. will be of use in preliminary screening of barley samples. There is potential for these new methods to be applied to malt anal.: both varietal identification of malts and detn. of the extent of (protein) modification. Components yielding processing problems can be identified and quantitated in malt samples.

ANSWER 46 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1986:570903 CAPLUS

DOCUMENT NUMBER:

105:170903

TITLE:

Molecular comparison of alcohol-soluble wheat and

buckwheat proteins

AUTHOR(S):

Skerritt, J. H.

CORPORATE SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE:

Cereal Chemistry (1986), 63(4), 365-9 CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE:

Journal

LANGUAGE:

Enalish

Comparisons of buckwheat and wheat proteins according to amino acid compn., electrophoresis, and immunol. reaction revealed little or no similarities. Whereas most of the material extd. from wheat flour by 70% EtOH (following salt extn.) was protein in nature, similar exts. from buckwheat contained only 2.4% N. Unlike wheat gliadin, the corresponding buckwheat fraction was rich in lysine, arginine, and glycine; it was not electrophoretically resolvable into gliadinlike bands on lactate-buffered polyacrylamide gels, and on SDS polyacrylamide gels; it had only minor components in the gliadin mol. size range. Immunol. studies with rabbit polyclonal and mouse monoclonal antibodies showed little cross-reactivity between cereal prolamins and buckwheat proteins. Celiac sera with high IgG anti-gliadin titers also reacted very weakly with buckwheat proteins. These results suggest that alc.-sol. buckwheat proteins (which are only minor components of the endosperm) bear little mol. similarity to wheat prolamins; descriptions of the former as glutenlike are misleading.

ANSWER 47 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1986:49930 CAPLUS

DOCUMENT NUMBER: TITLE:

104:49930 A sensitive monoclonal-antibody-based test

for gluten detection: choice of primary and secondary

antibodies

AUTHOR(S):

Skerritt, John H.; Diment, John A.; Wrigley,

Colin W.

CORPORATE SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, NSW 2113,

Australia

SOURCE:

Journal of the Science of Food and Agriculture (1985),

36(10), 995-1003 CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE:

English

Of a series of monoclonal antibodies prepd. to cereal proteins, 2 antibodies with specificity for low-mobility, heat-stable prolamins in wheat and related cereals were investigated as possible probes for a test for gluten in cooked or processed foods. Urea-based solvents were superior to iso-PrOH or SDS extractants in allowing sensitive detection of trace amts. of prolamins. The antibodies detected bread and durum wheat and rye prolamins most strongly, followed by barley then oats; detection of corn and rice was quite weak. This selectivity is suitable for a test for prolamins toxic to coeliac-disease patients. Several enzyme-labeled 2nd

antibodies, for detection of monoclonal antibody bound to cereal protein, were unsuitable reagents since an appreciable fraction of the 2nd antibodies bound directly to the cereal proteins. Sensitive, artifact-free detection of antibody binding could be performed using the peroxidaseantiperoxidase technique or by direct conjugation of horseradish peroxidase to the monoclonal antibodies.

ANSWER 48 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1986:49929 CAPLUS

DOCUMENT NUMBER:

104:49929

TITLE:

A sensitive monoclonal-antibody-based test for gluten detection: quantitative immunoassay Skerritt, John H.

AUTHOR(S):

CORPORATE SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, NSW 2113,

Australia

SOURCE:

Journal of the Science of Food and Agriculture (1985),

36(10), 987-94 CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE:

Journal

LANGUAGE:

English

An enzyme-coupled monoclonal antibody has been used to quantify gliadin-like immunoreactivity in a variety of foods. Small discs of nitrocellulose are soaked in food ext. or a series of std. gliadin solns., and incubated with antibody and an enzyme substrate yielding a sol. product. By use of a photometer, std. curves for gliadin may be constructed and the apparent gliadin content of samples calcd. The reproducibility of the procedure was examd. using a variety of common foods and food proteins. The limit of detection for wheat gliadin was .apprx.20 .mu.g/mL ext.; gliadin levels in excess of this value were found in some gluten-free bread mixes and starch [9005-25-8] sources. The overall time for anal. is 5-6 h, although for large nos. of samples, overnight blocking of non-specific antibody binding may be used. It is possible that a library of enzyme-linked monoclonal antibodies could be developed as useful tools for specific food anal.

ANSWER 49 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

1986:49928 CAPLUS

104:49928

TITLE:

A sensitive monoclonal-antibody-based test for gluten detection: studies with cooked or

processed foods

AUTHOR(S):

Skerritt, John H.; Smith, Robyn A.

CORPORATE SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, NSW 2113,

Australia

SOURCE:

Journal of the Science of Food and Agriculture (1985),

36(10), 980-6 CODEN: JSFAAE; ISSN: 0022-5142 Journal

DOCUMENT TYPE:

English

LANGUAGE:

A method for detection of wheat, rye, barley and oat proteins in a wide range of foods, including baked goods and processed meats has been developed. The procedure requires immobilization of food exts. on nitrocellulose paper followed by treatment with an enzyme-conjugated monoclonal antibody. Upon addn. of the appropriate enzyme substrate, gluten-contg. foods yield purple spots; a wide range of non-gluten common food proteins did not react. The method has several advantages over other means of detecting cereal protein, such as electrophoresis. It is rapid, requiring little sample prepn., and does not require sophisticated equipment or prior knowledge of electrophoretic patterns of common non-cereal food proteins. Since the method may be used with cooked or baked foods, it should be suitable for food-monitoring applications.

ANSWER 50 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1986:33153 CAPLUS

NGUYEN 09/830,876

DOCUMENT NUMBER:

104:33153

TITLE:

Detection and quantitation of cereal protein in foods using specific enzyme-linked monoclonal

antibodies

AUTHOR(S):

Skerritt, John H.

CORPORATE SOURCE: SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia Food Technology in Australia (1985), 37(12), 570-2

CODEN: FTAUAC; ISSN: 0015-6647

DOCUMENT TYPE:

LANGUAGE:

English.

A simple test for the presence and level of cereal gluten proteins in foods has been developed using monoclonal antibodies with specificity for heat-stable proteins from wheat, rye, barley, and oat grain. The test is faster, more sensitive and more reliable than other methods, such as electrophoresis, and may be applied to both cooked or processed as well as raw foods. The ability of monoclonal antibodies to act as sensitive reagents having reproducible specificities should allow their use in a wide range of immunochem. methods in food anal.

ANSWER 51 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1985:59452 CAPLUS

DOCUMENT NUMBER:

102:59452

TITLE:

Monoclonal antibodies to gliadin proteins

used to examine cereal grain

protein homologies

AUTHOR(S):

Skerritt, John H.; Smith, Robyn A.; Wrigley, Colin W.; Underwood, P. Anne

CORPORATE SOURCE:

Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE:

Journal of Cereal Science (1984), 2(4), 215-24

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE:

Journal Enalish

LANGUAGE:

Monoclonal antibodies were prepd. to a gliadin protein ext. of bread wheat (Triticum aestivum cv Timgalen) and specific antibody -cereal protein interactions were detected using horseradish peroxidase-coupled second antibodies after transfer of proteins to nitrocellulose following electrophoresis. Whereas some antibodies had broad specificity for gliadin protein, other antibodies of narrower specificity were investigated further. latter antibodies were selective for .omega.-gliadins and bound neither high-mol.-wt. glutenin subunits albumin and globulin wheat proteins, nor a wide variety of other proteins. However, certain related cereal species such as durum wheat, barley, and rye contained endosperm proteins recognized by these monoclonal antibodies. This observation confirms that sequence homologies exist between prolamins from wheat and related cereal species as well as between certain gliadins from hexaploid wheat.

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L16 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2000:335649 CAPLUS

DOCUMENT NUMBER:

132:333681

TITLE:

Detection of preharvest sprouting in cereal grains by

immunoassay of .alpha.-amylase

INVENTOR(S): PATENT ASSIGNEE(S): Skerritt, John Howard

Quality Wheat CRC Limited, Australia

SOURCE:

PCT Int. Appl., 51 pp. CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE WO 1999-AU995 19991111 WO 2000028319 **A1** 20000518 W: AU, CA, JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE CA 2345403 20000518 CA 1999-2345403 19991111 EP 1137935 20011004 **A1** EP 1999-957719 19991111 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2002529735 T2 20020910 JP 2000-581446 19991111 AU 757926 В2 20030313 AU 2000-15341 19991111 PRIORITY APPLN. INFO.: AU 1998-7058 19981111

WO 1999-AU995

A two-site immunoassay for the qual. or quant. detection of .alpha.-amylase in a test sample comprises: (i) exposing the test sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .alpha.-amylase under conditions permitting binding; (ii) subsequently exposing bound .alpha.-amylase to a second ("detection") antibody or antibody fragment which specifically or preferentially binds to a second epitope on the .alpha.-amylase that is distinct from the first epitope, under conditions permitting binding of the second antibody or its fragment to the bound .alpha.-amylase; and (iii) detecting any binding of the second antibody or its fragment to the bound .alpha.-amylase, wherein either of the first or second epitopes is an epitope comprising one or more of the amino acid sequences: IDRLVSIRTRGQIHS, CRDDRPYADG, or VNWVNKVGGS and variants thereof showing .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay is useful for detecting weather damage (i.e., preharvest sprouting) in cereal grain. Thus, a rapid tube sandwich ELISA detected .alpha.-amylase in preharvest-sprouted wheat exts. at .apprx.4 ng/mL.

268202-94-4 268202-95-5 268202-96-6

RL: ANT (Analyte); ANST (Analytical study) (detection of preharvest sprouting in cereal grains by immunoassay of .alpha.-amylase)

268202-94-4 CAPLUS

L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutaminyl-L-isoleucyl-L-histidyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

19991111

PAGE 2-B

PAGE 3-A

RN

268202-95-5 CAPLUS
Glycine, L-cysteinyl-L-arginyl-L-alpha.-aspartyl-L-arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-alpha.-aspartyl- (9CI) (CA INDEX CN

Absolute stereochemistry.

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PAGE 2-A

RN 268202-96-6 CAPLUS

CN L-Serine, L-valyl-L-asparaginyl-L-tryptophyl-L-valyl-L-asparaginyl-L-lysyl-L-valylglycylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

REFERENCE COUNT:

THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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Rice alpha-amylase
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       \begin{array}{c} 3.3 & 3.3 & 3.3 & 3.3 & 3.4 & 4.4 & 4.4 & 4.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 & 7.4 
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  Propionibacterium
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Eucalyptus grandis
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Human ORRX protein
Harbicidally activ
LXR alpha ligand b
Steroid hormone re
Maize partial RNA-
Retinoic acid rece
XR2 Homo sapiens
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RESULT 1
AAY93371
The present sequence represents an epitope from the wheat alpha-amylase Antibodies which recognise the epitope are used in a two-site immunoassay for qualitative or quantitative detection of alpha-amylase in a test sample. The assay is used for detecting weather damage in a cereal grain. Weather damage is caused by the action of hydrolytic
                       enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate the breakdown of starch granules and protein in the endosperm of germinating grain. Individual growers can identify areas of sprouting prior to harvest, preventing contamination of sound wheat by weather damaged wheat. The damaged grain can be harvested separately from the sound grain and financial losses resulting from down grading the whole crop can be avoided. The two-site immunoassays can be applied at mill or silo (elevator) receival of grain or can be used on farms with minima
                                                                                                                                                                                                                                                  Two site immunoassay for the qualitative or quantitative detection of alpha-amylase in a test sample, used to detect weather damage in a cereal grain, such as wheat, rye, triticale or bariey -
                                                                                                                                                                                                                                                                                                                                         Skerritt JH;
                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY93371 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epitope; wheat; alpha-amylase; two-site immunoassay; weather damage;
                                                                                                                                                                                                                                                                                                                                                                  (QUAL-) QUALITY WHEAT CRC LTD
                                                                                                                                                                                                                                                                                                             2000-376655/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      grain
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                                                                                                                                                                                                                          52pp; English
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AAP70595
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AAR94169
ABG31014
ABB57053
AAW03326
ABP60036
AAR74738
AAW752980
AAR52980
AAR52980
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Human ubiquitous n
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RESULT 2
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Best Local (
                                                  Matches
                                                                                                                                      The present sequence represents a wheat alpha-amylase. Antibodies which recognise epitopes from this protein are used in a two-site immunoassay for qualitative or quantitative detection of alpha-amylase in a test sample. The assay is used for detecting weather damage in a cereal grain. Weather damage is caused by the action of hydrolytic enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate the breakdown of starch granules and protein in the endosperm of germinating grain. Individual growers can identify areas of sprouting prior to harvest, preventing contamination of sound wheat by weather damaged wheat. The damaged grain can be harvested separately from the sound grain and financial losses resulting from down grading the whole or silo (elevator) receival of grain or can be used on farms with minimal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93374 standard; protein; 425 AA
                                                                                                                                                                                                                                                                                                                                           Two site immunoassay for the qualitative or quantitative detection alpha-amylase in a test sample, used to detect weather damage in a cereal grain, such as wheat, rye, triticale or barley - \frac{1}{2}
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                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cereal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epitope; wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence a wheat alpha-amylase.
                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (QUAL-) QUALITY WHEAT CRC LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase;
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86.7%;
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Pred. No.
                                                               Score 58; I
Pred. No. 0.
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                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 27-30; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gene expression system containing the promotor region of alpha-amylase gene, useful for mass production of a desired gene product in a plant host cell
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                                                                      Alpha-amylase; promoter; rice; monocot; cereal; brewing.
                                                                                                                           Rice alpha-amylase (alpha-Amy7-C gene product).
                                                                                                                                                                21-JAN-2002
                                                                                                                                                                                                       AAM50251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice alpha-Amy7-C protein SEQ ID
                                                                                                                                                                                                                                                                                                                                     359
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                                                                                                                                                                (first entry)
Location/Qualifiers
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71.4%;
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                                                                                          transgenic plant;
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01-AUG-1995;
08-OCT-1997;
22-NOV-1994;
  Unidentified
                                                                                                             31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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N-PSDB; AAI70537.
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95US-0509962.
97US-0947201.
94US-0343380.
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The present sequence is that of rice (Oryza sativa) cv. M202
alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C
(see AA170537). Expression of alpha-Amy7-C in cultured suspension
cells of rice was induced 6-fold at day 12 after sugar depletion,
and continued to increase up to day 14. The invention relates to
the use of an alpha-amylase gene promoter and signal sequence in
the production of recombinant proteins in transgenic plants and
transgenic plant seeds. In a claimed method, a transgenic monocot
is obtained by: transforming an immature embryo of the plant via
Agrobacterium-mediated transformation with DNA comprising a plant
calpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that
is induced under sugar-depleted or sugar-free conditions, a signal
peptide sequence, and an exogenous sequence encoding a gene product;
plant, which expresses the gene product under sugar-depleted or
sugar-free conditions. The gene product may also be obtained by
cultivating an anglosperm host cell. The transgenic monocot plants
are especially useful in brewing and to produce glucose from starch.
Alpha-amylase; promoter; expression vector; rice
                                                                         Alpha-amylase related protein #1.
                                                                                                                                                                                                                                                                                                           AAB97245 standard; Protein; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 61-64; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a transgenic monocot plant comprising a transgene under
control of an alpha amylase promoter and signal peptide sequences
provides transgenic plants particularly cereals for the brewing
industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..25
/label= Signal_peptide
26..428
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB Pred. No. 5; 1; Mismatches
                                                                                                                                                                                                                                                                                                           AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
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RRESULT 6
AAR7620
ID AAR78
XX AAR78
XX AAR7
XX AAR7
XX A1p)
XX
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Best Local s
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a gene expression system comprising the alpha-amylase gene promoter. DNA encoding the signal peptide of alpha-amylase and the promoter along with the glucuronidase reporter gene and hygromycin resistance gene are used in the construction of a GUS gene expression vector, which when transformed into rice suspension-cultured cells, can be used to investigate the expression of the vector under the control of the promoter. The gene expression system can be used to conduct gene regulation and protein expression and secretion using the characteristics of the alpha-amylase gene promoter and the DNA sequence encoding the signal peptide. The present sequence represents an alpha-amylase related protein used in the course of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene expression system comprising the promoter region of alpha-amylase gene, produces large quantities of alpha-amylase in culture medium of sugar starved rice - \,
                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ľ
                                                                                                                                                                                                                                                  Oryzae
                                                                                                                                                                                                                                                                                                           Alpha-Amy-6-C;
                                                                                                                                                                                                                                                                                                                                              Alpha-amylase-7-C
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR76520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76520 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 8; 104pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NASC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-1992;
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 Misc-difference
                                                                                                                  Misc-difference
                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1996
                                       Misc-difference
                                                                            Misc-difference
                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-167365/17.
)B; AAH20283.
                                                                                                                                                                                                                                                                                       expression system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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                                                                                                                                                                                                                                                  sativa
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10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IERLVSIRNRQGIH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDRLVSIRTRGQIH 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                           amylase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97TW-0101436.
 /note=
233
                                                                            /note=
218
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158
                                     /note=
224
                                                                                                                                                                                         Location/Qualifiers 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.6%;
71.4%;
                                                                                                                                  "corresp.
                                                                                                                                                                     "corresp.
                 "corresp.
                                                       "corresp.
                                                                                            "corresp.
                                                                                                                                                                                                                                                                                                         promoter; vector; heterologous;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB Pred. No. 5; 1; Mismatches
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                     CGG
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                                                                                                                                                                         codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 428;
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Query Match
Best Local S
Matches 10
26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
17-FEB-1989;
05-MAY-1989;
08-JUN-1989;
22-OCT-1990;
16-JAN-1991;
                                                                                                                                                                                                                                Virus; recombination; plant virus; alpha trichosanthin; phenotype; alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus; rice necrosis virus tobamovirus; gene expression; chinese cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR76519-R76521 represent the amylase gene products alpha-amylase-6-C, alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter regions of these amylase genes are used in a new gene expression system the system may be used for the expression of heterologous genes in plantage and for the large scale production of the encoded products of succession and for the large scale production of the encoded products of successions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene expression system contg. alpha-amylase gene promoter in plants for expression of heterologous genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                       AAR55130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP07143895-A
                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entered,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-236472/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NASC-) NAT
                                                                                                                          31-JUL-1992;
                                                                                                                                                   31-MAY-1994
                                                                                                                                                                             US5316931-A
                                                                                                                                                                                                                                                                                     Rice alpha-amylase coding
                                                                                                                                                                                                                                                                                                               25-MAR-2003
12-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                 AAR55130 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 IERLVSIRNRQGIH
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 27-30; 42pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDRLVSIRTRGQIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                               (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no acids in this sequence appear to have been wrongly feature table and the corresp. DNA file AAQ92806,
 89US-0347637.
89US-0363138.
90US-0600244.
91US-0641617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑĄ,
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294
                                                        89US-0310881.
                                                                                 88US-0160766
88US-0160771
                                                                                                                          92US-0923692
                                                                   88US-0219279
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                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     373
                                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded products of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 8
AAR32987
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Best Local S
Matches 10
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(Updated on 25-MAR-2003 to correct PF field.)
                                              (DAWS/)
(DONS/)
(GARG/)
(GRAN/)
(GRIL/)
(TURP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dawson
Turpen
 Donson
                                                                                                                                                              01-AUG-1991;
                                                                                                                                                                                               31-JUL-1992;
                                                                                                                                                                                                                              18-FEB-1993.
                                                                                                                                                                                                                                                              W09303161-A1.
                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                        Recombinant products; commercial production; fermentation;
blosynthesis; natural products; recombinant proteins;
product expression; protein expression; expressed proteins
                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003 (updated)
17-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR32987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1991;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                           Rice alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Columns 53-56; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant plant viral nucleic acid - capable of systemic infection and stable expression of non-native nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOS-) BIOSOURCE GENETICS CORP.
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DB; AAQ65574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364
                         ) DAWSON W O.
) DONSON J.
) GARGER S J.
) GRANTHAM G L.
) GRILLE L K.
) TURPEN A M.
) TURPEN T H.
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10; Conserv
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDRLVSIRTRGQIH 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IERLVSIRNRQGIH 377
Dawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Donson J,
Turpen TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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91US-0739143
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Ŏ.
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Grantham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB Pred. No. 5.1; Mismatches
GL,
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Turpen
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5.1;
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TH,
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Turpen
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ΑĀ,
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Garger
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SJ;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is rice alpha amylase. The coding sequence was inserted into a recombinant plant viral nucleic acid which was then used to express a recombinant product (in this case rice alpha-amylase) in a plant. The plant viral sequence may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean mottle, rice necrosis, geniniviruses, tomato golden mosaic, Cassava latent and maize streak viruses.
A DNA sequence (AAT47095) codes for rice alpha-amylase (AAW10469) novel viral nucleic acids can be constructed in which the alpha-amylase coding sequence is placed under control of the promoter of the tobacco mosaic virus coat protein gene, which has been deleted. The recombinant viral nucleic acid is capable of self-
                                                                                                                                                                                                                                Recombinant viral nucleic acid producing, e.g. male sterility in plants - comprises nucleic acid whose transcription is controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant plant viral nucleic acids - e.g. antibody or IL-1 in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-076518/09
N-PSDB; AAQ37680.
                                                                                                                                                       Example 4; Page 127-129; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640867-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus; TMV; rice; alpha-amylase; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW10469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW10469 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 96; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grille LK;
                                                                                                                                                                                                           another sequence
                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOS-) BIOSOURCE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 
(Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                    1997-065181/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 IERLVSIRNRQGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IDRLVSIRTRGQIH 14
                                                                                                                                                                                                                                                                                                                                                                                     AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                               AAT47095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Donson
Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0483502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US09299
                                                                                                                                                                                                                                                                                                                                                                                        TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to correct PN field.)
to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB:
Pred. No. 5.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                Grantham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                express a
                                                                                                                                                                                                                                                                                                                                                                                                                Grill
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ARESULT 1
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XX 25-
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replication, plants, and d tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant virus; alpha-haemoglobin; human; chinese cucumber; alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin; subgenomic promoter; coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                   subgenomic promoter, and a sequence encoding a plant virus coat protein. These heterologous sequences are preferably under the control of the native promoter sequence. By using a plant virus
                                                                                            The sequences given in AAW11868-71 represent proteins which were produced by the recombinant viruses of the invention. The viruses are recombinant plant viruses which comprise a native plant virus subgenomic promoter, at least one non-native plant virus
                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                Recombinant viral DNA for altering plant phenotype or protein prodn - contains non-native sub-genomic promoter for expression of heterologous protein and native promoter for expression of coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1991;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1989;
31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-1989;
05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5589367-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW11871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW11871 standard; Protein; 434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dawson
                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1990;
16-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1988;
15-JUL-1988;
  existing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                              1997-076845/07.
DB; AAT61377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                              4; Column 49-52; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSOURCE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||||| | ||
| IERLVSIRNRQGIH 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDRLVSIRTRGQIH 14
    cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , encapsidation and systemic spread in infected tobacco directs expression of the alpha-amylase in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-0310881.
89US-0347637.
89US-0363138.
92US-0923692.
88US-0160766.
88US-0160771.
88US-0219279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0600244.
91US-0641617.
91US-0737899.
91US-0739143.
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  native promoter sequence. can be altered with a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0184237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Granthan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB :
    coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                     a plant virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ę,
       without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 11
AAY01375
ID AAY01
XX Recc
KW Recc
KW trait
XX AAY01
XX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           involving germ cell. The recombinant viruses are stable and can cause systemic infection, with stable expression/transcription in plants that are hosts for the non-native part of the vector. The nucleotide sequences encoding these protein preferably integrated in plant viruses having either the O-coat protein or the U1-coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1989;
31-JUL-1992;
19-JAN-1994;
26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1988;
15-JUL-1988;
22-OCT-1990;
16-JAN-1991;

    sativa alpha-amylase

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-2003
04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY01375 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5889190-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY01375;
                                                                                                                                                       Recombinant plant viral nucleic single stranded RNA plant virus
                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                Dawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-FEB-1989;
05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant; plant virus; coat protein; systemic infection; transcription; therapeutic; rice; alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated
                                                                                                  Example
                                                                                                                                         products
                                                                                                                                                                                                                                         WPI; 1999-243290/20
                                                                                                                                                                                                                                                                              Turpen
                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated
                                                                                                                                                                                                                                                                                                                                       (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 IERLVSIRNRQGIH
                                                                                                                                                                                                                                                                              AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.
                                                                                                  4;
                                                                                                                                                                                                                      AAX29144.
                                                                                                                                                                                                                                                                                                                                       BIOSOURCE TECHNOLOGIES
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                                                                                                                                         in a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 AA;
                                                                                                  Columns 47-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
25-MAR-2003
                                                                                                                                                                                                                                                                            Turpenth;
                                                                                                                                                                                                                                                                                                  Donson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0184237.
88US-0160766.
88US-0160771.
88US-0219279.
90US-0600244.
                                                                                                                                                                                                                                                                                                                                                                            91US-0641617.
91US-0737899.
91US-0739143.
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89US-0347637
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92US-0923692.
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                                                                                                                                                                                                                                                                                                  Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
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                                                                                                46pp;
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Pred.
                                                                                                                                                                                                                                                                                                                                           INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                               acid derived from
- useful for the
                                                                                                  English.
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                                                                                                                                                                                                                                                                                                    Grantham GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           field.)
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5.1;
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                                                                                                                                                                                                                                                                                                      Grill LK;
                                                                                                                                                               a plus sense,
transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                               of
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The invention relates to a recombinant plant viral nucleic acid derived from a plus sense, single stranded RNA plant virus. The recombinant plant viral nucleic acid comprises: (a) a first plant viral subgenomic promoter that is native to the plus sense, single stranded RNA plant virus and

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RESULT 12
AAW84383
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                         31-JUL-1992;
26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
17-FEB-1989;
05-MAY-1989;
08-JUN-1989;
22-OCT-1990;
16-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                operably joined to a first nucleic acid expression sequence; and (b) a second plant viral subgenomic promoter that is non-native and is operably joined to a second nucleic acid expression sequence; where, (i) (a) and (b) are incapable of recombination with one another, (ii) either the first or the second nucleic acid expression sequence is a plant viral coat protein coding sequence. The recombinant plant viral nucleic acid allows the transcription of products in a host, such as therapeutic and other useful polypeptides or proteins e.g. enzymes, complex biomolecules and ribozymes. It also gives the option of applying the coding sequence to the desired organism, tissue, organ or ceil, is stable for the foreign coding sequences and is capable of systemic infection in the plant host. The transformation and regeneration of target organisms become
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice; alpha-amylase;
systemic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999
Recombinant plant viral vector - that is capable of systemic infection in host plant and stable production of heterologous DNA useful for producing therapeutic proteins for treating e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice alpha-amylase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW84383 standard;
                                                                                                                                                                                                                 (BIOS-) BIOSOURCE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                          26-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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                                                                                                             1999-142035/12
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434
                                                                                                                                                Donson J,
Turpen TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                      9205-0923692
8805-0160771
8805-0160771
8805-0119279
8905-0310881
8905-0310881
9005-0347637
8905-0347637
9105-0600244
9105-0641617
9105-0719143
9405-0719143
9405-0719143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; plant virus; RNA plant virus promoter;
foreign gene expression; AIDS therapeutic drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.6%;
71.4%;
                                                                                                                                                                       Garger SJ, Granthan GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB Pred. No. 5.1; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                                                                                                                         Grill LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 13
AAW807792
ID AAW807792
XX AAX807
XX AAX87
XX Enter XX En
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Best Local :
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                                                                                                                                                                                                                                                                                                          26-JUL-1991;
01-AUG-1991;
31-JUL-1992;
                                                                                                                                                                               Garger
Donson
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Animal RNA virus; viral coat protein; plant; male sterility; interleukin; EPO; erythropoietin; CSF; colony stimulating factor; Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine; stereo specific catalysis; alpha-amylase; rice.
                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                       (BIOS-) BIOSOURCE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1990;
16-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1989;
08-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY87792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                     2000-338510/29.
DB; AAA12394.
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10; Conserv
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milarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 AA;
                                                                                                                                                                                                    Grill LK,
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                                                                                                                                                                                                                                                                                                    8905-0310881

8905-0363138

8805-0160766

8805-0160727

8805-022279

8805-0347637

9005-0347637

9005-0547637

9105-0737899

9105-0737899

9105-0737899
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                                                                                                                                                                                                    Turpen
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5.1;
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                                                                                                                                                                                                    GL,
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                                                                                                                                                                                                       Dawson WO,
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Recombinant non-retroviral nucleic acid for producing proteins such interleukins, melanin and vaccines, comprises subgenemic promoters linked to sequences coding for viral coat protein and heterologous

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AAY35541

ID AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used
                                                                                                                                                        AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                    Page 1288-1289; Disclosure;
                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST )
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sinusitis; purulent otitis media; erythema
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97FR-0014673
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5.1;
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RESULT 15
AAU31870
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Q
                                                                                The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated converted to the polypeptide. The polypeptides are also useful for converted to the polypeptide and to them. Cells converted to the proteins are useful for identifying a therapeutic agent converted to a pathology related to aberrant expression or converted to the protein converted to the protein converted to the nucleic acids encoding the polypeptide. Vectors comprising converted to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful proliferation; to regulate haematopoiesis; and in the converted to the protein and can be used as nutritional supplements. They may be used to converted the protein and proliferation; to regulate haematopoiesis; and in the cartilage, tendon and/or nerve tissue growth or regeneration; to converted to the protein and proliferation; as anti-inflammatory agents; and converted to the protein and proverted to the prov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy {	ext{-}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted
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                                       sequences
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26-JAN-2001;
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stem cell proliferation; haematopolesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                              immune suppression and/or stimulation; as antin treatment of leukaemias. AAU29510-AAU33304
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                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Page 521; 765pp; English.
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8; Conserv
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                                           of novel
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2001US-0770160.
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57.1%;
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                                           represent the amino the invention.
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Query Match

58.9%;

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and CC antidabetic activity and acts as an angiogenesis and vascularization and the invention is useful for treating CC regulator. An antisense molecule of the invention is useful for treating CC retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood cyan countries and development of tissues, tissue regeneration and organ cand tissue repair in a subject. The products of the invention are useful CC for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-x protein contribution. This sequence represents the human VEGF aprotein protein and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-x protein protein and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-x protein protein and organ repair by promoting any protein activity or vascularization.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 12; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-442669/38.
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163 MDRLLQLRSRNETHS 177
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, Xu J;
                                Conservative
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                         CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has coulmbrary, cytostatic, antirheumatic, antiarthritic, antiparoriatic and candidabetic activity and acts as an angiogenesis and vascularization cregulator. An antisense molecule of the invention is useful for treating corpreventing cancer; rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate cartivity and development of tissues, tissue regeneration and overland to the invention of new blood vascularization including formation and proliferation of new blood cyanularization including formation and proliferation of new blood cyanularization including formation and proliferation of new blood cyanularization and development of tissues, tissue regeneration are useful corpreparing medicaments for treating wounds such as dermal ulcers, corpressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, corpressure sores, the tissue repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein corposite the method of the invention.
                                                            Query Match
Best Local S
Matches 6
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                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 26; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing dises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating preventing diseases associated with inappropriate anglogenesis active such as cancer, rheumatoid arthritis, psoriasis and wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV
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18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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   2 DRLVSIRTRGQIHS
                                                         Similarity 6; Conserv
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                                                                                                                                                                               168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sprengel JJ,
, Xu J;
                                                            Conservative
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99US-0124967.
99US-0164131.
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                                                                                     57.5%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yon
                                                            Score 42; DB Pred. No. 6.4; 5; Mismatches
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activity
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preventing dise such as cancer,

22-DEC-1998; 18-MAR-1999; 08-NOV-1999;

21-DEC-1999; 29-JUN-2000. WO200037641-A2

Homo sapiens.

Query Match Best Local S Matches 6

Similarity 6; Conserv

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Sequence

167

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Best Local
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                                                                                                                                                                                                      This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an antiagenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting anglogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote this great troubs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostati antirheumatic; antiarthritic; antipsoriatic; antiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10653 standard;
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                                                                                                                                               skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or vascularization. This sequence represents the human VEGF-X protein derived from clone 20 which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 12;
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18-MAR-1999;
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                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV
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i SN,
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47
                                                        Similarity 6; Conserv
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ERIITVSTNGSIHS
                         DRLVSIRTRGQIHS
ERIITVSTNGSIHS
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                                                        Conservative
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99US-0124967.
99US-0164131.
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42.9%;
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60
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                                                                        Score 42;
Pred. No.
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                                                                     DB
12;
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                                                                                      Length 282;
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AAX59286
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                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ48600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998;
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269..274
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234..240
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281..29
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51..57
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34..39
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23..29
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153..1
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15..23
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Novel cDNA encoding human bone morphogenic proteins, vectors, cells and methods of recombinant production, useful for diagnotreatment of, e.g. bone disorders $\,\cdot\,$ ectors, host diagnosis ar and

Claim 11; Page 184-185; 187pp; English.

by standard recombinant methodology. Determining the presence or absence of a mutation in the polynucleotides or determining the presence or amount of expression of the polypeptides is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject. The polynucleotides can also be used to prevent, treat or ameliorate a medical condition. The proteins are useful for diagnosis and/or treatment of diseases associated with BMPs, in particular bone disorders (e.g. osteoarthritis, cartilage defects and tissue repair), and in particular for stimulation of angiogenesis. The polynucleotides are useful as reagents for differential identification of tissues or celements are useful as reagents. The invention provides novel human bone morphogenic proteins (BMP) and nucleic acids encoding the BMPs. The BMP polypeptides can be expressed biological samples. The polynucleotides can be used absence

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sequence

gene therapy

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rapy to promote the growth of endothelial cells. The present represents a BMP of the invention (clone HSYAE36).

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RESULT 2
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                                                                                                                                                                                      The sequence represents the amino acid sequence of novel human protein, NHP #3, isolated from a human adremal gland cDNA library. NHP nucleotides are useful for drug screening and clinical trial monitoring, and for the diagnosis and treatment of physiological or behavioural disorders, cancer and infectious disease. Nucleotide constructs encoding functional NHPs, mutant NHPs, as well as antisense and ribozyme molecules can also be used in gene therapy for the modulation of NHP expression. NHP polypeptides may be used to produce agonists, antagonists and antibodies for the regulation of NHP expression in the treatment and/or diagnosis of
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding novel human proteins (NHP), useful for treating physiological or behavioural disorders, cancers and infectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turner CA,
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29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02751 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Novel Human Protein clinical trial monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious disease; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Human
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)B; AAS03539.
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47
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6; Conserv
                                                                   h 57.5%;
Similarity 42.9%;
6; Conservative
                   DRLVSIRTRGQIHS 15
ERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                      Page 62; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donoho G,
                                                                                                                                         305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 AA;
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llarity 42.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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99US-0162547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy.
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physiological disorder; behavioural disorder;
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Pred. No. 12;
5; Mismatches
                                                                 Score 42; DB 22; Length 305; Pred. No. 13; 5; Mismatches 3; Indels
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RESULT 21
AAY84558
ID AAY84
The present sequence represents a human platelet-derived growth factor C (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have Ct the ability to stimulate and enhance proliferation or differentiation, CC and/or growth or motility of cells expressing a PDGF-C receptor. CPDGF-C polypeptides can be used in pharmaceuticals for promoting cell CC proliferation, preferably in combination with one other growth factor C and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and also be used, to promote fibroblast CC mitogenesis in a mammal and to induce PDGF alpha receptor activation. CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma CC and erythroleukemia, can be identified by testing for expression of PDGF-C antagonists can also be used to inhibit tissue cremodelling during invasion of tumour cells into a normal population of CC cells. Antagonists can also be used to treat fibrotic conditions, CC especially found in the lung, kidney or liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1998;
18-DEC-1998;
21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                                                                                                                                                                                                                                                                                                                                                        Novel DNA encoding differentiation, gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eriksson U,
Oestman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fragment of platelet-derived growth factor C (PDGF-C)
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1998;
12-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                             receptor
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DB; AAA12524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J, Aase K,
Heldin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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98US-0108109.
98US-0110749.
98US-0113002.
99US-0135426.
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                                                                                                                                                                                                                                                                                                                                                                                                          ng PDGF-C useful to stimulate or enhance proliferation,
growth and motility of cells expressing the PDGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by AAS"
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RESULT 22
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Query Match
Best Local
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Best Local
                                                                                                                                                                                                                Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58166 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; prolliferative disorder; wound healing; infectious disease.
                                                                                   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds an infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung
                                           Sequence
                                                                                                                                                          diagnostic or research purposes. The proteins may be used disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                       chromosome identification, as chromosome markers, and for numerous
                                                                                                                                                                                                    polynucleotide sequences may be used for detection of lung cancer,
                                                                                                                                                                                                                                                                                                                                                 Claim 11;
                                                                                                                                                                                                                                                                                                                                                                            antigens, useful for treatment,
such as lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer associated polypeptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                       cancer associated gene sequences, referred to as lung cancer
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)B; AAF18314.
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                Page 1305-1306; 1425pp; English.
                                           339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated protein; neuroprotective; cy
e; immunomodulatory; muscular active; vulnerary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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 57.5%;
42.9%;
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Pred.
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                          prevention, and
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 42;
No.
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              Length
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                                                                                                                                                                                                                                                                                                                                                                                    screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or anglogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue generation; regeneration; angiogenic disorder; age-related
                                                                                                                                                                                                                                                                                                  of
by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes the isolation of a novel human vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-580306/49
N-PSDB; AAZ23691.
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02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VEGF-E protein
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                                                                                                                                                                                          in mammals, by detecting abnormally high or low VEGF-E gene expression tissue samples. They can also be used to diagnose a disease or
                                                                                                                                                                                                                                                           of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders
                                                                                                                                                                                                                                                                                                                         vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New growth factor polypeptide useful endothelial disorders, e.g. cardiac
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98US-0184216.
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6; Conservative
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      The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ3438, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
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22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                                                                                 New secreted and transmembrane polypeptides and useful for treating blood coagulation disorders, adhesion disorders - \,
                                                                                                                                                                                                                                                                                   Wood
                                                                                                                                                        Claim 12; Fig 207; 530pp;
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RESULT 24
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27-JAN-1998;
05-JUN-1998;
                                                                                                                                                                                    Growth,
VEGF-R c
                                                                                                                                                                                                                             The present sequence represents a vascular endothelial growth factor related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antagonize its activity. VEGF-R antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
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                                                                                                                                                                                                                                                                                                                                                                      A vascular endothelial polynucleotide, useful
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                                                                                                                                                                                 angiogenesis and to treat coronary artery blockage. The
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                                                                            Similarity
6; Conserv
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                                             DRLVSIRTRGQIHS
                                                                                                                                                                                                                  cancer. VEGF-R itself can be used to stimulate tissue
                                                                                                                                                                                                                                                                                                                           Page
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98US-0088089.
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42.9%;
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Pred. No.
                                                                                          Score 42;
Pred. No.
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RESULT 26
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The invention relates to the human growth factor homologue zvegf4 (2) (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/PEGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human cyegf4 or fragments thereof, particularly human zvegf4/human zvegf4 conscience to fusions; expression constructs and host cells comprising human zvegf4 nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating the proliferation, differentiation, migration or method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to
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10-NOV-1999;
04-FEB-2000;
                        metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 48; Page 125-126; 143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth factor homologs and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilbert T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-687541/67
)B; AAC81582.
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99US-0164463.
2000US-0180169.
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present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids that encode them, ischemia, multiple sclerosis an
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AAB24250
ID AAB24
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                                                                                                                                                                                                                                     The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LP8 or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LP8 antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LP8 are useful for treating atherossis. The present sequence represents human LP8, which is also called VEGFh.
                 AAB44322 standard; Protein; 345
                                                                                                                                                                                                                                                                                                                                                                                                                               Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LPB or its analog and treating atherosclerosis by administering LPB antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 20
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; platelet derived growth factor related protein; LP8; VEGFh; vascular endothelial growth factor h; tissue regeneration; vulnera atherosclerosts; PDGF related protein; antiarteriosclerotto.
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2000; 2000WO-US06427
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DB; AAC64426.
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                                                                                                                                                  Similarity 6; Conserv
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                                                                                         ERIITVSTNGSIHS 60
                                                                                                                    DRLVSIRTRGQIHS 15
                                                                                                                                                                                                                                                                                                                                                                                                       Page 63-64; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERIITVSTNGSIHS
                                                                                                                                                                                                            345 AA;
                                                                                                                                                    Conservative
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Matches 6
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26-JUL-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                                                                                                                              AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polyneptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide to AAC7800 to AAC78907 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                Claim 12; Fig 207; 636pp; English.
                                                                                                                                                                                                                                                                                                                                         Novel PRO polypeptides and polynucleotides used in detection methods, to target bloactive molecules to specific cells, and to modulate cellular activities .
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen Goddard A, Godowski PJ, Grimaldi CJ, Gunney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000;
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                                                                                                      Sequence
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DB; AAC78582.
2 DRLVSIRTRGQIHS
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6; Conser
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sequence tag; detection; cancer.
                                                                                                      345
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9940-US28551
9940-US285551
9940-US31095
9940-US31095
9940-US31274
200040-US00219
200040-US00277
200040-US00376
                                             Conservative
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99US-0145698.
99US-0162506.
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                                                        57.5%;
                                            Score 42; DB Pred. No. 15; 5; Mismatches
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RESULT 29 AAB10633

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                                                                                                                                                                                                                                         This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration are useful for the invention are useful for the products of the invention are useful
                                                                                                                                                   skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity vascularization. This sequence represents the RACE generated human VE protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
                                                                                                                      Sequence
                                                                                                                                                                                                              for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 127pp; English.
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18-MAR-1999;
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DB; AAA71951.
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                           Ν
                                                         Similarity 6; Conserv
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ERITVSTNGSIHS
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                                                                                                                      345
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                                                         Conservative
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Pred. No.
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                                                           Mismatches
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                                                                                      Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gosiewska
                                                         Indels
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                                                                                                                                                                 activity or human VEGF-
                                                         Gaps
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2003,

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CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and CC antidiabetic activity and acts as an angiogenesis and vascularization CC regulator. An antisense molecule of the invention is useful for treating CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic CC retinopathy by inhibiting angiogenic activity or inappropriate CC vascularization including formation and proliferation of new blood CC vessels, growth and development of tissues, tissue regeneration and organ CC and tissue repair in a subject. The products of the invention are useful CC for preparing medicaments for treating wounds such as dermal ulcers, CC pressure sores, venous sores, diabetic ulcers and burns and to promote Skin graft growth, tissue repair poliferation of new blood vessels, consideration. This sequence repersents the human VEGF-X protein consideration in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10634
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18-MAR-1999;
08-NOV-1999;
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF-X; vascul
antirheumatic;
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า SN,
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6,
                          Similarity
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                                                                                                                                                      described in the method of
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Job time : 48.8571 secs

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3. /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/laa/backfiles1.pep:*
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Result No.

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Minimum Maximum

Database

RESULT 1 US-07-973-324A-4

ALIGNMENTS

Sequence 4, Application US/07973324A Patent No. 5460952

GENERAL INFORMATION:
APPLICANT: Yu, Su
APPLICANT: Liu, L

Yu, Su-May

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

STREET: Chicago

ADDRESSEE:

E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive

COUNTRY:

United States of America

Illinois

60606-6402

APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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Matches 10; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04 NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, MICHAEL F.
REFEISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 3114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/973,324
                                                                                                                CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/639,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312/474-0448
                                                                                                       APPLICATION NUMBER: US 01 FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 22-NOV
NAME: Gass, REGISTRATION
                                                      FILING DATE:
                                                                   APPLICATION NUMBER:
                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                Illinois
                                                                                                                                                                                                                                                                                                                                                                                                  233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                    NUMBER: US 07/973,324
04-NOV-1992
                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1994
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71.4%;
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Pred. No. 0.78;
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Best Query Match Matches

Local

. Similarity 10; Conserv

Conservative

61.6%; 71.4%;

Score 45; DB 1; Length 428; Pred. No. 0.78; 1; Mismatches 3; Indels

0;

TELEX: 25-3856
INFORMATION FOR SEQ ID NO:

REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447

APPLICATION NUMBER: FILING DATE: 04-NO CLASSIFICATION: 43

04-NOV-1992

US/07/973,324A

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE:

protein

RESULT 2 US-08-343-380-4

Sequence 4, Application US/08343380 Patent No. 5712112 GENERAL INFORMATION:

APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase (

Genes

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: marshall, O'Toole,
STREET: 6300 Sears Tower, 233

Gerstein, Murray & Borun South Wacker Drive

STATE: 1

8Y: United States 60606-6402

of America

CITY:

Chicago Illinois

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-072-917A-4
                                                                        ; MOLECULE TYPE: US-09-072-917A-4
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Best Local Similarity 71.4%;
Matches 10; Conservative
Query Match 61.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNET/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/3425
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMA
                                                                                                                                                                                      TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 606ub
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/072,917A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT:
                                                                                                              LENGTH: 428 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic TILE OF INVENTION: Plant Seeds MMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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TYPE: amino acid
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: Illinois
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233 South Wacker Drive/6300 Sears Tower
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Score 45; DB Pred. No. 0.78
1; Mismatches

    Mismatches

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0.78;
                                 DB 3; Length 428;
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Indels
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RESULT 5
US-07-923-692C-6
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; MOLECULE TYPE: US-07-923-692C-6
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Patent No.
GENERAL IN
                                                TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER C.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CTTY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING LALL.
PRIOR APPLICATION NUMBER: US 310,881
APPLICATION NUMBER: US 310,881
TO DATE: 17-FEB-1989
                                                                                                                                                                                                                                    FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-433-4150
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTUADER: Daton; in Ealose #1
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                                 TOPOLOGY:
                                                                                                                                                                       REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
REFERENCE/DOCKET NUMBER: USA
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-JA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 347,637 FILING DATE: 05-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                              : 434 amino acids
amino acid
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Garger, Stephen J
Grill, Laurence K
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Turpen, Thomas H.
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                                 linear
              protein
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08-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    JMBER: US 160,771
26-FEB-1988
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26-FEB-1988
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V: 435
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15-JUL-1988
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Best Local
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APPLICANT:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Garger, Stephen J. APPLICANT: Grill, Laurence K. TITLE OF INVENTION: RECOMBINA
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 16-JAN-FILING DATE: 16-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-432-777
                                                                                                                                                                                              APPLICATION NUMBER: US 30 FILING DATE: 05-MAY-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 16
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 923,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                 FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 31 FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                  APPLICATION NUMBER:
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2001 Ferry Building
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Dawson, William 0.
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26-FEB-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.68;
                                                                                                                                                                                                                                                                                 US 160,771
                                                                                                                                    US 219,279
                                                                                                                                                                                     US 363,138
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US 641,617
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                                                                                                                                                                                                                                 US 347,637
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                                                    BIOG-20121
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Pred. No. 0.79;
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RESULT 7
US-08-482-920-6
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GENERAL IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                FILING LATE:
PRIOR APPLICATION DATA:
OF THE PRIOR APPLICATION NIMBER: US 160,771
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-JAN-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 18
FILING DATE: 19-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patent in Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2
FILING DATE: 15-JUL-1988
                                                                                                                                                                                                                                                                                                       FILING DATE: 22-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                     FILING DATE: 05-MAY-PRIOR APPLICATION DATA:
                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08 FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 26-FEF
                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 17-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                       APPLICATION NUMBER:
                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                              FILING DATE:
                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donson,
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                                                                                                                                                                                     26-FEB-1988
                                                                                          05-MAY-1989
                                                                                                                                                                                                                                 17-FEB-1989
                                                                                                                                                                                                                                                                                                                         UMBER: US 600,244
22-OCT-1990
                                                                                                                                     26-FEB-1988
                                              08-JUN-1989
                                                                                                                                                                                                                                                                              16-JAN-1991
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                                                                                                                                                                                                                                                                                          US 641,617
                                                            US 363,138
                                                                                                                                                                                                 US 160,766
                                                                                                                                                                                                                                               US 310,881
                                                                                                                                                                                                                                                                                                                                                                                  US 184,237
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                 US 219,279
                                                                                                        US 347,637
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Pred. No.
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TELEPHONE: 415-854-3660
FILEPHAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
SOLECULE TYPE: protein
US-08-482-920-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-484-341-6
; Sequence 6, Application US/08484341
; SEQUENAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 817
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PS-ENDS (100, Ve
APPLICATION DATA;
APPLICATION DATA;
APPLICATION NUMBER: US/08/484,341
FILING DATE: OT-Jun-1955
PRIOR APPLICATION NUMBER: US/08/484,237
APPLICATION NUMBER: US/08/484,237
APPLICATION NUMBER: US/08/484,237
APPLICATION NUMBER: US/08/41,617
FILING DATE: 10-JAN-1990
APPLICATION NUMBER: US/08/41,617
FILING DATE: 17-FEB-1988
APPLICATION NUMBER: US/08/41,637
APPLIC
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Local Similarity 71.4%;
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 IERLVSIRNRQGIH 378
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TYPE: amino acid
TOPOLOGY: linear
HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-484-341-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
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APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Thomas H.
APPLICANT: Grantham, George L.
APPLICANT: Grant, Laurence K.
APPLICANT: Grantham, George S.
APPLICANT: Grantham, Grantham PLANT VIRAL NUCLEIC ACIDS
NUMBER OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-483-502-6
                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: EMP PC COMPATIBLE
COMPUTER: DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION NUMBER: US/08/483,502
FILING DATE:
APPLICATION NUMBER: US/08/483,502
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 2-COT-1990
PRIOR APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION NUMBER: US 641,617
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
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Best Local Similarity 71.4%;
Matches 10; Conservative
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FILING DATE: 26-FBB-1988
PRIOR APPLICATION DATA: US 160,771
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEPAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: 20005
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밁 Q

Matches Query Match

> 0; Gaps

0,

FILING DATE: 08-JUN-PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 219,279

APPLICATION NUMBER: US 363,138 FILING DATE: 08-JUN-1989

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APPLICANT: DAWSON, William O.
APPLICANT: DAWSON, William O.
APPLICANT: TURPEN, MAIN, GEORGE L.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: GRANGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS FILE REFERENCE: 0008010023CNUS01
CURRENT APPLICATION NUMBER: US/09/726,651A
CURRENT APPLICATION NUMBER: 08/483,502
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR APPLICATION NUMBER: 08/184,237
PRIOR APPLICATION NUMBER: 08/184,237
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR APPLICATION NUMBER: 07/600,244
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US-09-726-651A-6
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δ
                                                                                                                  ; OTHER INFORMATION: CLONE: alpha-amylase
; OTHER INFORMATION: protein
US-09-726-651A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Applic
Patent No. 6448046
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                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                       SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-962-481
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1991-07-26
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 07/737,899
                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     ENGTH: 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                          10;
    1 IDRLVSIRTRGQIH 14
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09726651A
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                                        Conservative
                                                                                                                                                                                                                                                                             for Windows Version 4.0
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71.4%;
                                                          61.6%;
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                                        Score 45; DB 4
Pred. No. 0.79;
1; Mismatches
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                                                                              DB 4;
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; LOCATION: 1...460
; OTHER INFORMATION: Xaa-unknown or other
US-09-198-452a-959
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Best Local S
Matches 8
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                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/09564595D Patent No. 6495668
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                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/564,595D CURRENT FILING DATE: 2000-05-03 PRIOR APPLICATION NUMBER: US 09/304,216 PRIOR FILING DATE: 1999-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
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                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gilbert, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                    OTHER INFORMATION: fusion polypeptide
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 460
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365 | IERLYSIRNRQGIH 378
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8; Conserv
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                   2 DRLVSIRTRGQIHS 15 : |:::: | | | | | | |
ERIITVSTNGSIHS
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57.1%;
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Pred. No.
                                                                                           Score 42; DB Pred. No. 2.1;
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1.3;
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                                                                                                                Length 302;
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GENERAL INFORMATION:

APPLICANT: Ferrara, Napoleone

APPLICANT: WO, Sophia S.

TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH EXCTOR AND BONE MORPHOGENETIC

TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,

TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION

FILE REFERENCE: P1122

CURRENT APPLICATION NUMBER: US/09/040,220D

CURRENT APPLICATION NUMBER: US/09/040,220D

CURRENT HING DATE: 1998-03-17

SEQ ID NO 2

LEGGH: AND ASSESSED IN NOS: 8

SEQ ID NO 2

LEGGH: AND ASSESSED IN NOS: 8

SEQ ID NO 2

LEGGH: AND ASSESSED IN NOS: 8
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APPLICANT: Glibert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1900-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILIN
RESULT 15
US-09-457-066-2
US-09-457-066-2
; Sequence 2, Application US/09457066
PATENT NO. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
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US-09-040-220D-2
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US-09-564-595D-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.9
Best Local Similarity 42.9
Matches 6; Conservative
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ORGANISM: Artificial Sequence
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47 ERIITVSTNGSIHS 60
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42.9%;
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Pred. No.
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2.4;
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APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
FILE REFERENCE: P1122P2
CURRENT APPLICATION NUMBER: US/09/265,686
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-03-17
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEG ID NOS: 8
SEG ID NO 2
LENGTH: 345
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Human
US-09-265-686-2
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US-09-540-224-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2
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CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 280
LENGTH: 345
                                                                                                                                                                                                                    Sequence 5, Application US/09540224 Patent No. 6468543 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
FILE REPETICATION NUMBER: US/09/540,224
CURRENT APPLICATION NUMBER: US/09/540,129
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
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Best Local
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APPLICANY: Sheppard, Paul O.
APPLICANY: Sheppard, Paul O.
APPLICANY: Sheppard, Paul G.
APPLICANY: Gilbertson, Debra G.
APPLICANY: Gest, James W.
APPLICANY: West, James W.
APPLICANY: Mest, James W.
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nes 6; Conserv
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Local Similarity 42.9%;
es 6; Conservative
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42.9%;
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
US-09-706-968-2
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                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Shemaker, Kimberly E.
APPLICANT: Shemaker, Kimberly E.
APPLICANT: Ghemaker, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV
FILL REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
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CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-564-595D-33
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09706968 Patent No. 6528050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 345
                                                                                                                                                                                                                                                              APPLICANT: Gao, Zeren APPLICANT: Hart, Chai APPLICANT: Piddington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gilbert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 345
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                              Hart, Charles E.
Piddington, Christopher S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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42.9%;
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42.9%;
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Pred. No.
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Pred. No. 2.4;
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                                                                                                                                                                      ZVEGF3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-2
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Best Local Similarity
Whiches 6; Conserve
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US-08-466-120-2
                                                                     RESULT 21
PCT-US94-07266-2
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                                                                                                                                                                                                                                               US-08-466-120-2
                                        Sequence 2, Application PC/TUS9407266 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08466120 Patent No. 5869284
                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 24 JUN 94
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,13
                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: IBM PS/2
OPERATING SYSTEM: WS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CAO, ET TITLE OF INVENTION:
             APPLICANT: CAO, ET AL. TITLE OF INVENTION: Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE,
ADDRESSEE: CECCHI, STEWART
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: LI
                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08, FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                396 KLVSLRTLSSVHS 408
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                                                                                                                                               2 DRLVSIRTRGQIHS 15
                                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                      AMINO ACIDS
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                                                                                                                                                                                                     53.4%;
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42.9%;
Retinoic Acid Receptor Epsilon 2
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                                                                                                                                                                                                    Score 39;
Pred. No.
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAIN, GILFILLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                    DB 2;
12;
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                                                                                                                                                                                                                    Length 433;
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Sequence 8, Application US/08333358

Patent No. 5571696

GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ORG MS., ESTELITA S.
APPLICANT: ORG MS., ATHONY E.
APPLICANT: GROMEYER Ph.D., UWE K.
APPLICANT: GROMEYER Ph.D., VINCENT NMN
APPLICANT: GROMEYER Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLECULE TYPE: PCT-US94-07266-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTOREY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,114
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                            COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMBUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 INCH DISKETTE
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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                             ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 So. Flower St., Suite 2000 CITY: Los Angeles
STREE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 53.4%;
Local Similarity 53.8%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Concur
RRENT APPLICATION DATA: US
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396 KLVSLRTLSSVHS 408
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  us/08/333,358
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 433;
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RESULT 23
US-08-463-694-8
Contence 8, Ar
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Patent No.
GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8849
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MANGELSOORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UME K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO MI., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                  APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 3192
REFERENCE/DOCKET NUMBER: P31 8936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 05-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                            TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 So. Flower St., Suite 2000
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Local Similarity 53.8%;
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SD
                                                                                                                                                                                                                                                         UMBER: US/08/463,694
05-JUN-1995
                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.25
                                                                                      31192
nee: P31 8936
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Pred. No.
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Best Local Similarity
7; Conserve
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APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELLTA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: ORO Ph.D., OWNE K.
APPLICANT: BORGMEYER Ph.D., UNDE K.
APPLICANT: YAO MI., TSO-PANG NMN
APPLICANT YAO MI., TSO-PANG NMN
APPLICANT YAO MI., TSO-PANG NMN
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-694-501-8
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                                                                                                                                  Matches
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 931 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/694,501
FILING DATE: 07-AUG-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: US/07/761,068
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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403 KLVSLRTLSSVHS 415
                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                            RLVSIRTRGQIHS 15
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                                                                                                                                                                                                                                                                                                                                                                                          440 amino acids
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                                                                                                                                                          Score 39;
Pred. No.
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                                                                                                                                                          DB 1;
12;
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                                                                                                                                                                                           Length 440;
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RESULT 25

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Moore, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,411A
FILING DATE: 18-NOY-1994
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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LENGTH: 443 amino acid
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIAO, Shutsung APPLICANT: SONG, Ching
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                            APPLICANT: Seol, Wongi
APPLICANT: Choi, Hueng-Sik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
77210-4433
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                                                                                                                                      CITY: Boston
STATE: MA
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                                                                                                                                                                      STREET:
                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 KLVSLRTLSSVHS 418
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                                                                                                     02110-2804
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                                                                                                                     USA
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                                                                                                                                                                                      Richardson P.C.
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Pred. No. 13;
3; Mismatches
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DB 3; Length 446, 13;

Indels

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Gaps

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; MOLECULE TYPE: protein US-08-372-652-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY, AGENT INFORMATION:
ATTORNEY, AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542,5070
                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/EP95/03247
APPLICATION UNMBER: UK 9413536.2
APPLICATION UNMBER: UK 9413536.2
ETILING DATE: 16-AUG-1994
ATTORNEY/ACENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION UNMBER: 32141
REFERENCE/DOCKET NUMBER: 300487.0402
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/776,844
FILING DATE: 24-JUN-1997
OLASSIFICATION: 536
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LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDMESS: not relevant
TOPOLOGY: linear
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ENMARK, EVA
APPLICANT: GUSTAFSSON, JAN
APPLICANT: GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TITLE OF INVENTION: TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 53.4%;
Local Similarity 53.8%;
nes 7; Conservative
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FILING DATE: 13-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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409 KLVSLRTLSSVHS 421
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single
linear
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                                                                                                                                                                                                                                                       TENCH: 446 amino acids
TYPE: anino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-325-2
    RESULT 29
PCT-US95-16311-3
; Sequence 3, Application PC/TUS9516311
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                                                                                                           В
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US-09-909-325-2
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Best Local Similarity 53...
""" Conservative
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Patent No. 6525188
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
                                                                                                                                                                                        Matches
                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   Local Similarity 53.8 es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/776,844
APPLICATION NUMBER: 08/776,844
EILING DATE: <Unknown>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,325
FILING DATE: 19-Jul-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUSTARSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                           409 KLVSLRTLSSVHS 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 KLVSLRTLSSVHS 421
                                                                                                                                            3 RLVSIRTRGQIHS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                      53.4%;
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Pred. No.
                                                                                                                                                                                                        Score 39; DB
Pred. No. 13;
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COUNTRY:

TELEFAX:

DB 4; Length 446; 3; Indels

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Query Match

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US-08-373-935-1
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Best Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILLING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30.162
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Mangelsdorf, David J.
APPLICANT: Willy, Patricia J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MOODE, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hueng-Sik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                              TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: 61,
TELEFAX: 200154
                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 7; Conserv
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TELEFAX: 617/542-8906
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                                                                                                               STATE:
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Pred. No.
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                                        Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                       ; MOLECULE TYPE: protein US-08-373-935-1
                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-4737
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                    TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                      FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                              NAME: Reiter, Stephen REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
410 KLVSLRTLSSVHS 422
                     3 RLVSIRTRGQIHS 15
                                                      Conservative
                                                                                                                                      linear
                                                                53.4%;
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Pred. No.
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Search completed: August 29, 2003, 18:44:39 Job time: 17.8571 secs

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Title:
Perfect score:
Sequence:
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No.
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   55
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113
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                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 Score
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   protein search, using sw
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1: /cgn2_6/ptodata/2/pub
2: /cgn2_6/ptodata/2/pub
3: /cgn2_6/ptodata/2/pub
4: /cgn2_6/ptodata/2/pub
5: /cgn2_6/ptodata/2/pub
6: /cgn2_6/ptodata/2/pub
6: /cgn2_6/ptodata/2/pub
6: /cgn2_6/ptodata/2/pub
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15: /cgn2_6/ptodata/2/pub
16: /cgn2_6/ptodata/2/pub
17: /cgn2_6/ptodata/2/pub
18: /cgn2_6/ptodata/2/pub
18: /cgn2_6/ptodata/2/pub
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73
1 IDRLVSIRTRGQIH
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Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 29, 2003, 18:42:11; Search time 23.5714 Seconds (without alignments) 87.043 Million cell updates/sec
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Maximum Match 100%
Listing first 100
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   61
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'cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
'cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
'cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
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'cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
'cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
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US-09-852-209A-19

5 US-10-131-600-19

5 US-10-103-197-5

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US-09-852-209A-5

US-09-925-302-776

US-09-925-303-2

US-09-925-303-2

US-09-923-995-4

US-09-923-995-4

US-09-923-995-488

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Sequence 6, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 776, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 488, App
                                                                                                                            Description
 US-09-998-182A-488
US-09-978-189-48
US-09-978-189-48
US-09-978-560A-488
US-09-978-558A-488
US-09-978-558A-488
US-09-978-564A-488
US-09-978-564A-488
US-09-978-193A-488
US-10-140-127-286
US-10-140-127-286
US-10-141-702-286
US-10-145-784-286
US-10-145-813-286
US-10-145-813-286
US-10-147-503-286
 sequence
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RESULT 2
US-09-852-209A-19
; Sequence 19, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Rice alpha-amylase US-10-280-679B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-10-280-679B-6
                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILLING DATE: 1992-07-31
PRIOR PELICATION NUMBER: 07/600,244
PRIOR FILLING DATE: 1990-10-22
PRIOR FILLING DATE: 1990-10-16
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILLING DATE: 1991-01-16
PRIOR PELICATION NUMBER: 07/737,899
PRIOR FILLING DATE: 1991-07-26
PRIOR FILLING DATE: 1991-07-26
PRIOR FILLING DATE: 1991-07-39,143
PRIOR FILLING DATE: 1991-08-01
PRIOR FILLING DATE: 1991-08-01
PRIOR FILLING DATE: 1991-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartice RNA virus Transformation Vectors
FILE REFERENCE: LSBC-0109-US03
CURRENT APPLICATION NUMBER: US/10/280,679B
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 09/557,941
PRIOR APPLICATION NUMBER: 08/484,341
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10280679B Publication No. US20030150019A1
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 07/310,881
PRIOR ELING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR FILING DATE: 1988-02-26
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TYPE: PRT
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les 10; Conserv
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71.4%;
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US-10-142-418-286
US-10-142-418-286
US-10-142-420-286
US-10-142-427-286
US-10-142-427-286
US-10-142-760-286
US-10-143-030A-488
US-10-143-030A-486
US-10-152-531-286
US-10-137-840A-286
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Pred. No.
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                                                                                                          APPLICANT: AASE, KATIN
APPLICANT: LEE, XUTİ
APPLICANT: PONTEN, ANDICA
APPLICANT: OUTELA, MATKO
APPLICANT: UUTELA, MATKO
APPLICANT: HELDIN, CATI
APPLICANT: HELDIN, CATI-HENTİK
APPLICANT: HELDIN, CATI-HENTİK
APPLICANT: HELDIN, CHTİSTET
TİTLE OF İNVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-ETİKSSON et al-1064-44740
CURRENT APPLICATION NUMBER: US/10/131,600
CURRENT FILING DATE: 1909-09-30
PRIOR APPLICATION NUMBER: 60/09/410,349
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/144,022
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US-10-131-600-19
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PRIOR FILLING DATE: 1999-09-30
PRIOR PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILLING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILLING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILLING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
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Best Local Similarity 42...
""" hes 6; Conservative
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 117
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 NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver.
SEQ ID NO 19
LENGTH: 117
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APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR (
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
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APPLICANT:
APPLICANT:
                                                                            PRIOR APPLICATION NUMBER: 60/144,022 PRIOR FILING DATE: 1999-07-15
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42.9%;
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Pred. No.
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APPLICANT: Young et al.

APPLICANT: Young et al.

TITLE OF INVENTION: Bone Morphogenic Proteins (BMP family)

FILE REFERENCE: P7012P1

CURRENT APPLICATION NUMBER: U9/10/103,197

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/488,690

PRIOR APPLICATION NUMBER: 09/489,690

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-07-15

PRIOR FILING DATE: 1999-07-15

VERTOR FILING DATE: 1998-07-15

NUMBER OF SED ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 297

TWYNEL DATE: DET
Sequence 5, Application US/09852209A
Patent No. US20020164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: ERIKSSON, Ulf
APPLICANT: HELE, Xuri
APPLICANT: DONTEN, Annica
APPLICANT: DUTELA, MARKO
APPLICANT: ALITALO, KARI
APPLICANT: HELDIN, CARI-Henrik
APPLICANT: BETSHOLTZ, Christeer
TITLE OF INVENTION: THEREFOR, AND USES THERROF
FILTE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
CURRENT ETLING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US/09/852,209A
CURRENT ETLING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION WUMBER: 60/113,002
PRIOR FILING DATE: 1999-15-21
PRIOR FILING DATE: 1999-15-21
PRIOR FILING DATE: 1999-5-21
PRIOR FILING DATE: 1999-15-21
PRIOR FILING DATE: 1998-17-18
PRIOR FILING DATE: 1998-17-18
PRIOR FILING DATE: 1998-17-18
PRIOR FILING DATE: 1998-17-18
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; ORGANISM: HOI
US-10-131-600-19
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US-10-103-197-5
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Best Local S
Matches 6
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Publication No. US20030032098A1
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9.6;
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US-10-131-600-5
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Publication No. US20030082670A1
GEMERAL INFORMATION:
APPLICANT: ERIKSSON, U1f
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 5
LENGTH: 318
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Best Local Similarity 42.5
Matches 6; Conservative
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42.9%;
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ALINALIZAMN: ERIAL.

PLICANN: LEE, Xuri
APPLICANN: LEE, Xuri
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APPLICANN: LEE, Xuri
APPLICANN: DONTEN, Annica
APPLICANN: OESTMAN, Arne
APPLICANN: DONTEN, Annica
APPLICANN: DONTEN, Annica
APPLICANN: DONTEN, Annica
APPLICANN: DONTEN, Annica
APPLICANN: DONTEN, Annica
APPLICANN: HELDIN, Carl Henrik
APPLICANN: BETSHOLIZ, Christer
FILIE OF INVENTION: PLETEREOR, AND USES THEREOF
FILE REFERENCE: 09-410349-ERIKSSON et al-1064-44740
CURRENT EILNG DATE: 1090-30
CURRENT FILING DATE: 1990-30
PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1999-12-18
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1999-12-18
PRIOR FILING DATE: 1999-12-18
PRIOR FILING DATE: 1999-12-18
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
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RESULT 7
US-09-925-302-776
Sequence 776, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
PIILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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Pred. No. 10;
5; Mismatches
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RESULT 9
US-09-818-943-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2
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US-09-823-033-2
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Best Local
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Patent No. US20020004225A1
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                APPLICANT: LI, HONG
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH
TITLE OF INVENTION: (PDGF-C) AND USES THEREOF
FILE REFERENCE: 1064/48487
CURRENT APPLICATION NUMBER: US/09/818,943
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/192,507
PRIOR PPLICATION NUMBER: US 60/192,507
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 7
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APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annic
APPLICANT: AASE, Karin
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-795-006A-149
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US-09-923-995-4
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Patent No. US20020081700A1
GENERAL INFORMATION:
                                                                                                                                                                           SEQ ID NO 149
LENGTH: 345
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Best Local Similarity 42.5
Matches 6; Conservative
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CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,164
PRIOR FILING DATE: 2000-08-07
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TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
FILE REFERENCE: 00-47
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PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
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SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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TYPE: PRT
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PRIOR FILING DATE: 1998-03-13 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-20 PRIOR PRIOR APPLICATION UNMBER: 60/078939 PRIOR APPLICATION UNMBER: 60/079294 PRIOR APPLICATION NUMBER: 60/079294 PRIOR APPLICATION NUMBER: 60/079294 PRIOR FILING DATE: 1998-03-25 PRIOR FILING DATE: 1998-03-26 PRIOR FILING DATE: 1998-03-26 PRIOR PRIOR PRIOR DATE: 1998-03-26 PRIOR APPLICATION NUMBER: 60/079656 PRIOR APPLICATION NUMBER: 60/079656	GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Botsein, David APPLICANT: Betan, Abpoleen APPLICANT: Eaton, Dan APPLICANT: Genomers, Luc APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Modder, Austin L. APPLICANT: Mapier, Austin L. APPLICANT: Mapier, Austin L. APPLICANT: Mapier, Mary A. APPLICANT: Mapier, Mary A. APPLICANT: Mapier, Mary A. APPLICANT: Pann, James, APPLICANT: Pann, James, APPLICANT: Pann, James, APPLICANT: Pann, James, APPLICANT: Wood, Williams, P. Mickey APPLICANT: Wood, Williams, P. M	RESULT 12 US-09-978-295A-488 ; Sequence 488, Application US/09978295A ; Patent No. US20020156006A1
PRIOR APPLICATION NUMBER: 60/082700 PRIOR FILING DATE: 1998-04-22 PRIOR PELING DATE: 1998-04-22 PRIOR PELING DATE: 1998-04-22 PRIOR APPLICATION NUMBER: 60/082796 PRIOR APPLICATION NUMBER: 60/082796 PRIOR APPLICATION NUMBER: 60/083336 PRIOR APPLICATION NUMBER: 60/083326 PRIOR PILING DATE: 1998-04-27 PRIOR APPLICATION NUMBER: 60/083322 PRIOR PILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29	APPLICATION N FILING DATE: APPLICATION N	PRIOR FILING DATE: 1998-03-27 PRIOR APPLICATION NUMBER: 66/079689 PRIOR FILING DATE: 1998-03-27 PRIOR PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27

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RESULT 13
US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60
FILING DATE: 1998-05-1
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APPLICATION NUMBER:
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/085323
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APPLICATION NITHTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. US20020169284A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
LENGTH: 345
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APPLICANT: UUTELA, Warko
APPLICANT: ALITALO, Kari
APPLICANT: OESTRAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
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PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
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CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
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APPLICANT: Baker Kevin P
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PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
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              Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                          Stewart, Timothy A.
                                                                         Roy, Margaret Ann
Shelton, David L.
                                                                                                        Paoni, Nicholas F
                                                                                                                         Pan, James;
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Kuo, Sophia S.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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Desnoyers, Luc
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Pred. No.
Transmembrane Polypeptides and
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CURRENT FILING DATE: P2630PLC27
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 05/05/250
PRIOR APPLICATION NUMBER: 05/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
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PRIOR PRIOR FILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/077450
PRIOR PRILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-11
PRIOR PELICATION NUMBER: 60/077641
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                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: p2630p1C9
CURRENT APPLICATION NUMBERS 777777
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CURRENT APPLICATION NUMBER: US/09/9 CURRENT FILING DATE: 2001-10-15 PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250
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OR APPLICATION NUMBER: 60/085700

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APPLICATION UNMBER: 60/085323
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Shelton, David L.
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Gao, Wei-Qiang
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079728
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DR APPLICATION NUMBER: 60/079920
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OR APPLICATION NUMBER: 60/077791

OR APPLICATION NUMBER: 60/078004

OR APPLICATION NUMBER: 60/078004

OR FILING DATE: 1998-03-13

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OR FILING DATE: 1998-03-20

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OR APPLICATION NUMBER: 60/078939

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OR APPLICATION NUMBER: 60/64249

OR FILING DATE: 1997-11-03

OR APPLICATION NUMBER: 60/065311

OR FILING DATE: 1997-11-13

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APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 PLICATION NUMBER: 60 LING DATE: 1998-04-

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APPLICANT: No., Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Williams, P. Mickey
APPLICANT: Winas, Daniel
APPLICANT: Williams, P. Mickey
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
ITITLE OF INVENTION: Acide Encoding the Same
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FILE OF INVENTION UNMBER: US/09/999,832A
CURRENT APPLICATION NUMBER: 09/91855
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/062250
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Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
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Goddard, Audrey
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Sophia S.
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sen, Mary E.
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J. Christopher
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FILING DATE: 1997-11-0 APPLICATION NUMBER: 60, FILING DATE: 1997-11-11 APPLICATION NUMBER: 60, FILING DATE: 1997-11-2 APPLICATION NUMBER: 60, FILING DATE: 1998-03-11 APPLICATION NUMBER: 60, FILING DATE: 1998-03-11 APPLICATION NUMBER: 60, FILING DATE: 1998-03-11 APPLICATION NUMBER: 60, FILING DATE: 1998-03-11 APPLICATION NUMBER: 60, FILING DATE: 1998-03-11 APPLICATION NUMBER: 60,	CANT: WOOD, WILLIAM OF INVENTION: Secre OF INVENTION: Secre OF INVENTION: Acid OF INVENTION: Acid OF INVENTION: Acid OF INVENTION: DATE: OF INVENTION UNMER: APPLICATION UNMER: FILING DATE: 2001 APPLICATION UNMER: FILING DATE: 1997-1 APPLICATION UNMER: FILING DATE: 1997-1 APPLICATION NUMBER:	Godowski Grimaldi Gurney, Hillan, Kijavin, Kuo, Sop Napier, Pan, Jam Paoni, Nam Paoni, Mar Shelton, Stewart, Tumas, D	RESULT 17 US-09-978-189-488 Sequence 486, Application US/09978189 Publication No. US20030004102A1 GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Baker Kevin P. APPLICANT: Desnoyers, Luc APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan APPLICANT: Ferrara, Napoleon APPLICANT: Filvaroff, Ellen APPLICANT: Frony, Sherman APPLICANT: Godor, Harspeter APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Geritsen, Mary E. APPLICANT: Geritsen, Mary E. APPLICANT: Gerber, Hanspeter	PRIOR APPLICATION NUMBER: 60/085579 PRIOR TILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085704 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLICATION NUMBER: 60/085704 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085704 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085704 PRIOR APPLICATION NUMBER: 60/085697 PRIOR APPLIC
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OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083499
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OR APPLICATION NUMBER: 60/08354
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BR APPLICATION NUMBER: 60/084598
OR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084627
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R APPLICATION NUMBER: 60, R FILING DATE: 1998-05-11 R FILING DATE: 1998-05-12 R APPLICATION NUMBER: 60, R FILING DATE: 1998-05-12 R APPLICATION NUMBER: 60, R FILING DATE: 1998-05-12 R FILING DATE: 1998-05-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMBER: 60-12 R APPLICATION NUMB
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/083322
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RESULT 18
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Best Local
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
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VENTION: SECRETED PROTEINS AND

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Pred. No. 11;
5; Mismatches
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; PRIOR FILING DATE: 2000-09-30; NUMBER OF SEQ ID NOS: 162; SEQ ID NO 6; LENGTH: 345; TYPE: PRT : ORGANISM: Homo sapiens US-09-796-753-6
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SEO ID NO 488
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-608A-488
RESULT 20
US-09-978-585A-488
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Best Local Similarity 42.9%;
Matches 6; Conservative
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEO ID NOS: 624
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\PPLICANT: Baker Kevin P.
                                                                                                                           Match 57.5%;
Local Similarity 42.9%;
es 6; Conservative
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                                                               47 ERIITVSTNGSIHS 60
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                                                                                       2 DRLVSIRTRGQIHS 15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Desnoyers, Luc
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er, Mary A.
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                                                                                                                             Score 42; DB
Pred. No. 11;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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                                                                                                                                                            DB 11; Length 345;
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US-09-978-191A-488
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APPLICANT: Baker Kevin P
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James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630F1015
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEO ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEO ID NO 488
LENGTH: 345
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-978-585A-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.5%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                            Sequence 488, Application US/09978191A Publication No. US20030050239A1
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                                                                                                                                                                                                                                                                                                                                                                                                     47 ERIITVSTNGSIHS 60
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                               Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Gao, Wei-Qiang
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Filvaroff, Ellen
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Eaton, Dan
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Grimaldi, J. C
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/978, CURRENT EILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 00/918585
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILLING DATE: 1997-10-17
PRIOR PRIOR PILLING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILLING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PILLING DATE: 1998-03-11
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PRIOR FILLING DATE: 1998-03-27
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Kuo, Sophia S.
Napier, Mary A.
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Tumas, Da
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OR APPLICATION NUMBER: 60/081229

OR FILING DATE: 1998-04-09

OR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/084637
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Query Match Best Local S Matches 6

57.5%;

Score 42; DB pred. No. 11; 5; Mismatches

PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

RESULT 22
US-09-978-403A-488
US-09-978-403A, Application US/09978403A
; Sequence 488, Application US/0997840A1
; publication No. US20030050240A1
; publication No. US20030050240A1
; publication No. US20030050240A1

APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin Pa APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan

Ferrara, Napoleon Filvaroff, Ellen Botstein, David Desnoyers, Luc Eaton, Dan

Gerber, Hanspeter Gerritsen, Mary E.

Wei-Qiang

Goddard, Audrey
Godowski, Paul J.
Gorlmaldi, Paul J.
Gurney, Austin L.
Gurney, Austin L.
Hillan, Kenneth J
Hillan, Kvar J.
Kijavin, Tvar J.
Kijavin, Tvar J.
Kuj. Sophia S.
Kuo, Sophia S.

paoni, Nicholas F. Roy, Margaret Ann Shelton, David L.

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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-28
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
FILE REFERENCE: P2630PlC25
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Kljavin, Ivar J.
Kuo, Sophia S.
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Grimaldi, J. Christopher
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Goddard, Audrey
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Desnoyers, Luc
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
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APPLICATION NUMBER: 60/081229
TITING DATE: 1998-04-09
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APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/065311
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PRIOR PAPLICATION NUMBER: 60/081817

PRIOR FILING DATE: 1986-04-15

PRIOR PRIOR PAPLICATION NUMBER: 60/08195

PRIOR PRIOR PAPLICATION NUMBER: 60/08195

PRIOR PRIOR PAPLICATION NUMBER: 60/08256

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APPLICANT: ROUTL, MACHICLES F.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
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APPLICATION NUMBER: US/09/981,915A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/063311
PRIOR APPLICATION NUMBER: 60/065311
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OR APPLICATION NUMBER: 60/085579
OR PILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/08580
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Similarity 42.9%;
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Pan, James;
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Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
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NUMBER: 60/077632	DATE	RIOR

PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-21
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082706
PRIOR APPLICATION NUMBER: 60/082707
PRIOR APPLICATION NUMBER: 60/082707
PRIOR PRIOR FILING DATE: 1998-04-22
PRIOR PRIOR FILING DATE: 1998-04-22
PRIOR PRIOR FILING DATE: 1998-04-23
PRIOR PRILING DATE: 1998-04-23
PRIOR PRILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/08349
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PRIOR PRILING DATE: 1998-04-29
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PRIOR PRILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08466
PRIOR PRILING DATE: 1998-05-05
PRIOR PRILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR APPLICATION NUMBER: 60/08463
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PRIOR APPLICATION NUMBER: 60/08663
PRIOR PRIOR PRINCE: 1998-05-07
PRIOR APPLICATION N

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APPLICANT: Williams, P. Mickey
APPLICANT: William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263001C14
CURRENT APPLICATION NUMBER: US/09/978.824
CURRENT APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/06250
PRIOR RILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR RILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR REPLICATION NUMBER: 60/077632
PRIOR REPLICATION NUMBER: 60/077641
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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OR APPLICATION NUMBER: 60/085704
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                APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077791
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Tvar J
Kuo, Sophia S.
Napier, Mary A.
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f, Ellen
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PRIOR ETILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078930
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/08107
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OR APPLICATION NUMBER: 60/07
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60/082804

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OR APPLICATION NUMBER: 60/084441
DR FILING DATE: 1998-05-06
DR APPLICATION NUMBER: 60/084637
DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084639
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DR APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/085580
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
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FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/0
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-22
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FILING DATE: 1998-05-15
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-13
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APPLICATION N
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Desnoyers
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Shelton, David L.
Stewart, Timothy
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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o. US20030060406A1
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PRIOR APPLICATION NUMBER: 60/078939
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RESULT 28
US-09-978-423A-488
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; Sequence 188, Application US/09978423A
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1907-10-17
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OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/077450
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Baker Kevin P.
Botstein, David
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Shelton,
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Tumas, Daniel
Tumas, P. Mickey
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ton, David L.
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PRIOR APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081049 APPLICATION NUMBER: FILING DATE: 1998-0: FILING DATE: 1998-0: APPLICATION NUMBER: FILING DATE: FILING DATE:
APPLICATION 1 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: FILING DATE: 1998-03 FILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-03 APPLICATION NUMBER: 60/081203 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/079923 APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-04-23 APPLICATION NUMBER: FILING DATE: 1998-04 APPLICATION NUMBER: APPLICATION NUMBER: 60/082569 APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 APPLICATION NUMBER: FILING DATE: 1998-04 FILING DATE: FILING DATE: FILING DATE: APPLICATION FILING DATE: APPLICATION NUMBER: 60/080328 FILING DATE: 1998-03-31 APPLICATION NUMBER: FILING DATE: 1998-03-31 APPLICATION NUMBER: FILING DATE: 1998-04 FILING DATE: APPLICATION NUMBER: 60/082700 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/081819 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 APPLICATION NUMBER: NUMBER: NUMBER: 60/079920 NUMBER: 60/079689 1998-03-27 NUMBER: 60/081838 1998-04-15 NUMBER: 60/081817 1998-04-15 1998-04-1998-04-22 1998-04-1998-04-22 1998-04-1 1998-04-15 1998-04-09 1998-04-09 1998-04-08 1998-04-01 1998-04-01 1998-04-01 1998-03-33 1998-03-30 1998-03-27 1998-03-27 1998-04-21 1998-04-01 1998-03 1998-03-30 60/083336 4-27 60/080107 60/079664 60/082796 60/082804 60/082704 60/082568 60/081955 60/081229 60/081071 60/080334 60/080333 60/080327 60/080194 60/080165 60/080105 60/079786 60/082797

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FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

IUMBER: 60/083392 1998-04-29

APPLICATION NUMBER:

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RESULT 29
US-09-978-193A-488
; Sequence 488, Application US/09978193A
; Publication No. US20030073624A1
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Best Local Similarity
Matches 6; Conserv
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OR APPLICATION NUMBER: 60/084633
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OR APPLICATION NUMBER: 60/08349
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OR PILING DATE: 1998-04-30
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OR APPLICATION NUMBER: 60/083742
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OR PILING DATE: 1998-04-30
OR APPLICATION NUMBER: 60/08441
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FILING DATE: 1998-04-29
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5; Mismatches
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APPLICANT: WOLLTIAMS, F. MICKEY
APPLICANT: WOLD, WILLIAM I.
APPLICANT: WOLD, WILLIAM I.
APPLICANT: WOLD, WILLIAM I.
APPLICANTON: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: P2630P1C6

CURRENT FILING LOATE: 2001-07-30

PRIOR PEPLICATION UNMEER: 09/91855

PRIOR PEPLICATION UNMEER: 09/91855

PRIOR PEPLICATION UNMEER: 60/02220

PRIOR PEPLICATION UNMEER: 60/02220

PRIOR PEPLICATION UNMEER: 60/065311

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PRIOR PRILING DATE: 1998-03-20

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APPLICANT:
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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams, P. Mickey
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Gerritsen, Mary E.
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J. Christopher
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PR APPLICATION NUMBER: 60/080334

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/081070

DR APPLICATION NUMBER: 60/081049

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DR FILING DATE: 1998-04-08
                                                                                  DR FILING DATE: 1998-04-23

R APPLICATION NUMBER: 60/083336

DR FILING DATE: 1998-04-27

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/083392

DR APPLICATION NUMBER: 60/083495

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DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-08
DR FILING DATE: 1998-04-09
DR APPLICATION NUMBER: 60/08129
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DR APPLICATION NUMBER: 60/08129
DR APPLICATION NUMBER: 60/08125
DR FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/083496
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
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Sequence 488, Application US/09999830A
Publication No. US20030077700A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
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US-09-999-830A-488
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084639
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DR FILING DATE: 1998-04-29
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DR APPLICATION NUMBER: 60/084366
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DR APPLICATION NUMBER: 60/084414
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A;Molecule type: mRNA
A;Residues: 379-389,'T',391-392,'D',394-429 <HUA>
A;Cross-references: GB:K02636; NID:g166992; PIDN:AAA32932.1; PID:g166993
A;Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase C;Genetics: <A56>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A94535
A;Accession: B30759
A;Status. ---
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A; Molecule type: DNA
A; Residues: 1-429 <RAH>
A; Residues: 1-429 <RAH>
A; Cross references: EMBL:X15227; NID:g18899; PIDN:CAA33299.1; PID:g295805
A; Cross references: embL:X15227; DID:g18899; PIDN:CAA33299.1; PID:g295805
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A:Map position: 6
A;Introns: 29/3; 346/3
A;Introns: 29/3; 346/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-A;Pathway: glycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: aleurone cell; germination; glycosidase; hydrolase;
F;172-318/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain Himalaya gene Amy46 for alpha-amylase R;Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S. J. Mol. Appl. Genet. 2, 579-588, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Khursheed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
A;Title: Barley alpha-amylase genes. Quant.
A;Reference number: A92700; MUID:89066691;
A;Accession: B31960
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A;Residues: 1-104,'G',106-154,'A',156-160,'pD',163,'G',167-196,'V',198-342,'T',344-392,
A;Cross-references: GB:J04202; NID:g166984; PIDN:AAA98615.1; PID:g166985
A;Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B
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                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 29/3; 346/3
C; Genetics: <A46>
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A; Residues: 1-51 <KHU>
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A;Cross-references: EMBL:M17125; NID:g166978; PIDN:AAA32926.1; PID:g166979
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A; Residues: 1-11, 'LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: Amy56
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                                                                                                                                                                                                                                                                                          A;Gene: Amyl
                                                                                                                                                                                                                                                                                                                          Genetics: <AA1>
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                                                                                                                                               catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
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A; ACCESSION. C. DNA ACCESSION E type: DNA A; Residues: 1-133, 'D', 135-424, 'Q', 426-427 < RAH> A; Residues: 1-133, 'D', 135-424, 'Q', 426-427 < RAH> A; Cross: references: EMBL: X15226; NID: g18894; PIDN: CAA33298.1; A; Cross: references: gene Amy152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2 C;Species: Hordeum vulgare (barley) C;Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999 C;Accession: A31960; A00847; JE0405; A26267; A24457; A30759 R;Khursheed, B.; Rogers, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: aleurone cell; carbohydrate metabolism; germination; glycosidas
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A;Reference number: A92837; MUID:85159405; PMID:6335720
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C;Species: Hordeum vulgare (barley)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change
                                                                                                                   Plant Mol. Biol. 12, 119-121, 1989
A;Tittle: Nucleotide and predicted
A;Reference number: JE0405
A;Accession: JE0405
                                                                                                                                                                                                                                                                                                       R;Rogers, J.C.
J. Biol. Chem. 260, 3731-3738, 1985
A;Title: Two barley alpha-amylase gene families are regulated differently A;Reference number: A00847; MUID:85131184; PMID:3871776
A;Accession: A00847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. BIOl. Chem. 263, 18953-18900, 1900
A;Title: Barley alpha-amylase genes. Quantitative comparison
A:Reference number: A92700; MUID:89066691; PMID:3264283
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                                                                                                                                                                                        A; Experimental source: seed R; Rahmatullah, R.J.; Huang, J.K.; Clark, Plant Mol. Biol. 12, 119-121, 1989
                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-133,'D',135-194,'HRL',198-424,'Q',426-427 <ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-427 <KHU>
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A; Residues: 1-153 <HUA>
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11; Conserv
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Pred. No.
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Pred. No.
                                                                                                                                                                       amino acid sequences
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0.011;
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                                                                                                                                                                                                                    G.R.; Chandra,
                                                                                                                                                                       of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                        PID:g295804
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C; Superlamit
C; Keywords:
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k;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Hordeum vulgare (barley)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change
C;Accession: C21826
k;Huang, J;K; Swegle, M; Dandekar, A.M.; Muthukrishnan, S.
J, Mol. Appl. Genet. 2, 579-588, 1984
A;Accession: C21826
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C21826
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A,Rosidues: 1-133,'V',135-184,'A',186-366,'GA' <CHA>
A;Experimental source: cv. Himalaya
A;Experimental source: cv. Himalaya
A;Note: the authors translated the codon GTC for residue 134 as G1y
R;Svensson, B; Mundy, J; Glbson, R.M.; Svendsen, I.
Carlsberg Res; Commun. 50, 15-22, 1985
A;Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.
A;Reference number: A24457
A;Accession: A24457
A;Accession: A24457
A;Accession: A24457
A;Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-135 <HUA>
A;Cross:references: GB:K02635; NID:g166990;
C;Comment: The authors translated the codon
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A; Introns: 29/3; 344/3
A; Note: multigene family
C; Function:
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A;Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels A;Reference number: A26267
A;Accession: A26267
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11; Conserv
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                                  IDRLVSVSTRHGIHS 80
                                                                                                                                                           69.98;
larity 73.38;
Conservative
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73.3%;
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Pred. No. 0.03
1; Mismatches
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0.035;
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CAA for residue 47 as Pro and
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0.036;
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                                                                                                                                                           0;
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C;Superfamily: chalcone
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A; Residues: 1-428 <HUA>
A; Cross-references: EMBI
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A; Residues: 1-365 < KUN>
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C.Accession: A69580;
C.Accession: A.M.;
C.V.;
Caldwell, B.;
Capuano, V.;
Carter, N.M.,
C.;
Bron, S.;
Brusillet, S.;
Bruschl, C.V.;
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$10013
alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OS92) - rice
c;Species: Oryza sativa (rice)
c;Species: Oryza sativa (rice)
c;Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
c;Accession: $10013
R;Huang, N.; Sutliff, T.D.; Litts, J.C.; Rodriguez, R.L.
Plant MO1 Biol: 14, 655-668, 1990
A;Title: Classification and characterization of the rice alpha-amylase multigene fami
A;Reference number: $10013
A;Recession: $10013; MUID:91346657; PMID:2102847
A;Accession: $10013
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A; Introns: 30/3; 75/1; 345/3
C; Function:
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ce: var. M202
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                                                                                                                                                                                                                                                                                           61.68;
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                                                                                                                                                                                                                                  Score 45; DB 2; Pred. No. 1.8; 1; Mismatches
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RESULT
E72023
                        A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: E72023
                                                                                                                                                     oxygen-independent coproporphyrinogen III oxidase CP0977 [imported] - Chlamydophila C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: E72023; H81517
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C;Superfamily: oxygen-independent coproporphyrinogen oxidase
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A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coproporphyrinogen III oxidase [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 23-Mar-2001 C;Accession: G86601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.I. Mol. Gen. Genet. 221, 235-244, 1990
A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and A;Reference number: $12775; MUID:90318322; PMID:2370848
A;Accession: $12775
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                                                                                                    R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-458 <STO>
A;Cross-references: GB:BA000008;
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A; Residues: 1-434 < ONE>
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C; Species: Oryza sativa (rice)
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Best Local
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preliminary
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Similarity 71.4%;
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8; Conserv
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57.1%;
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J138
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Pred. No.
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                                                                                                                                                     R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ng arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                            A; Reference number: A99139
A; Accession: C90464
                                                                                                                                                                                                                                                                C;Date: 24-May-2001 #sequence_revision
C;Accession: C90464
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  A; Molecule type:
A: Residues: 1-666
                                                                                                                                A; Description: Sulfolobus
                                                                                                                                                                                                                                                                                                                    hypothetical protein acsA-9 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                          C90464
                                                   A;Status: preliminary
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and A;Reference number: A81500; MUID:20150255; PMID:10684935 A;Accession: H81517
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
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                                                                                                                                                                                                                                                                                                   A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: D87683
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein CC3502 [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
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A;Experimental source: strain AR39, HL cells
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A; Residues: 1-458 < REA>
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A; Residues: 1-45
                                                                                                                                                                              A; Gene:
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                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                    A;Cross-references: GB:AE005673; NID:g13425228; PIDN:AAK25464.1; GSPDB:GN00148
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A; Residues: 1-151 <STO>
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Best Local S
Matches 9
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9; Conser
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50.0%;
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57.1%;
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Pred. No.
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solfataricus complete genome

24-May-2001 #text_change 15-Jun-2001

Thi-Ngoc,

Awayez, M. goc, H.P.;

В δõ

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A;Gene: rplQ
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50S ribosomal protein L17 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AH2812 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 R;Kuthors; Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
                                                            A; Gene: AGR_C_3516
A; Map position: circular chromosome
C; Superfamily: Escherichia coli ribosomal protein L17
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A;Residues: 1-141 <KUR>
A;Residues: 1-141 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE006641; NID:g13816221; PIDN:AAK42970.1; GSPDB:GN00155 C;Genetics: A;Genetics: A;Gene: acsA-9 C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology
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A;Experimental source: strain C58 (Dupont)
                                                                                                                        A;Cross-references: GB:AE007869; PIDN:AAK87683.1; PID:g15157042; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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Best Local S
Matches 9
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Best Local :
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 6; Conservative
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              54.8%;
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40.0%; Pred. No.
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   6;
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                Score 40; I
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ed. No. 4.6;
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A56043
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S59771
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Best Local
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nes 9; Conserv
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8; Conserv
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R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, J.

R;Melson, Septola

R;Melson, S5971

R;Molecule type; DNA

A;Residues: 1-443 <NEL>
A;Residues: 1-443 <NEL>
A;Cross-references: EMBL:U32445; NID:g914969; PID:g914977; MIPS:YPR106w
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C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Paccesion: E75481
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smlth, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smlth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Accession: E75481
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-246 KMID
A.Residues: 1-246 KMID
A.Residues: 1-246 KMID
A.Experimental source: Strain R1
A.Experimental source: Strain R1
steroid hormone receptor-like protein RLD-1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999 C;Accession: A56043
R;Apfel, R.; Benbrook, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfahl, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YPR106w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein P8283.9

C;Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998

C;Accession: S59771
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C;Superfamily: conserved hypothetical protein HI0860
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l; Mismatches
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8.5;
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       G.; Pfahl, M.
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retinoid X receptor interacting protein No.15 - mouse C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_c
C;Accession: 149021
R;Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-65, 1995
A;Title: Isolation of proteins that interact specifically A;Reference number: A57664; MUID:95280959; PMID:7760852
A;Accession: 149021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
C; Superf
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A;Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive A;Reference number: A56043; MUID:95021230; PMID:7935418
A;Accession: A56043
A;Cross references: EMBL:U20389; NID:g665941; PIDN:AAA69522.1; A;Experimental source: Sprague-Dawley, hepatic R;Song, C.; Kokontis, J.M.; Hiipakka, R.A.; Liao, S. Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994 A;Title: Ubiquitous receptor: a receptor that modulates gene ac A;Reference number: I59264; MUID:95062154; PMID:7971966 A;Accession: I59264
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F;76-366/Domain: erbA transforming protein homology <ERBA>
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A; Residues: 1-445 <APF>
                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-446 <RES>
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I59354
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A; Cross-references: EMB
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Pred. No.
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Pred. No.
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       Matches
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A;Cross-references: GDB:389570; OMIM:600380
A;Map position: 19q13.3-19q13.3
C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: steroid hormone receptor F;85-381/Domain: erbA transforming protein homology <ERBA>F;87-154/Domain: DNA binding #status predicted <BIN>
                                                                                                                                                                                                                                                A; Cross-references: GB:U07132; NID:g641961; PIDN:AAA61783.1; A; Experimental source: osteosarcoma cells SAOS-2/BI0 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-447 <RES>
A;Residues: 1-447 <RES>
A;Cross-references: EMBL:U22662; NID:g726512; PIDN:AAA85856.1; PID:g726513
A;Cross-referently: unassigned erbA-related proteins; erbA transforming protein
C;Keywords: zinc finger
C;Keywords: zinc finger
F;96-367/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: I38975
R;Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J. Genes Dev. 9, 1033-1045, 1995
A;Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway A;Reference number: I38975; MUID:95262897; PMID:7744246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: vagina C;Superfamily: unassigned erbA-related proteins; erbA transforming protein C;Keywords: DNA binding; zinc finger C;Keywords: DNA binding; zinc finger E;76-366/Domain: erbA transforming protein homology <ERBA>
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A;Molecule type: mRNA
A;Residus: 1-32,'V',34-51,55-218,'V',220-446 <RE2>
A;Cross-references: EMBL:U14533; NID:g565661; PIDN:AAA52361.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  steroid hormone-nuclear receptor NER - human
(;Speckes: Homo sapiens (man)
(;Speckes: Homo sapiens (man)
(;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
(;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
(;Accession: JC4014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                 A;Title: NER, a new member of the gene family encoding the A;Reference number: JC4014; MUID:95011628; PMID:7926814 A;Accession: JC4014
                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-461 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Shinar, D.M.; Endo, N
Gene 147, 273-276, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: I38975
A;Status: preliminary
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                                                                                                                                                                                                                             A; Gene: GDB: UNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.; Rutledge, S.J.; Vogel, R.; Rodan,
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Conservative

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RESULT 22

S57596

ribosomal RNA processing protein RRP5 - yeast (Saccharomyces cerevisiae)

ribosomal RNA processing protein YM9529c

R;Alternate names: protein YM9529c

C;Species: Saccharomyces cerevisiae

C;Species: Saccharomyces cerevisiae

C;Accession: S57596; S72446

R;Skelton, J; Churcher, C.M.

submitted to the EMBL Data Library, June 1995

A;Reference number: S57597

A;Accession: S57597

A;Accession: S17596

A;Polecule type: DNA

A;Residues: 1-1729 < SKRE>
A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; PIDN:CAA90200.1; PID:g887610; MIPS:YMR229d

A;Cross-references: EMBL:249939; NID:g887599; 
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$46034

Nypothetical protein YBR163w - yeast (Saccharomyces cerevisiae)
hypothetical protein YBR163w - yeast (Saccharomyces cerevisiae)
hypothetical protein YBR1262

C; Species; Saccharomyces cerevisiae
C; Species; Saccharomyces cerevisiae
C; Accession: $46034

C; Accession: $46034

R; Fintlan, K.D.; Koetter, P.; Rose, M.; Becker, J.; Grey, M.; Li, Z.; Niegemann, E.; Sc
S; Gruenbein, R.; Hedges, D.; Kiesau, P.; Korol, S.; Krems, B.; Proft, M.; Siegers,
S.; Gruenbein, R.; Hedges, D.; Kiesau, P.; Korol, S.; Krems, B.; Proft, M.; Siegers,
S.; Gruenbein, R.; Hedges, D.; Kiesau, P.; Korol, S.; Krems, B.; Proft, M.; Siegers,
S.; Gruenbein, R.; Hedges, D.; Kiesau, P.; Korol, S.; Krems, B.; Proft, M.; Siegers,
S.; Gruenbein, R.; Hedges, D.; Kiesau, A.; Reseau, R.; Siegers, S.; Gruenbein, S.; Klolecule to the Protein Sequence Database, August 1994
A; Rocession: $46013
A; Accession: $46013
A; Accession: $46013
A; Rocession: $46014
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A;Gene: SGD.DEM1; MIPS:YBR163w
A;Cross-references: SGD:SO000367
A;Map position: 28
C;Superfamily: Saccharomyces cerevisiae
C;Superfamily: Saccharomyces
                                                                                                                                                                        A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1729 A;Pesidues: 1-1729 A;Cross-references: EMBL:Z49939; NID:9887599; PIDN:CAA90200.1; PID:9887610
A;Cross-references: EMBL:Z49939; NID:9887599; PIDN:CAA90200.1; PID:9887610
A;Cross-references: SGD:S0004842; MIPS:YMR229c
A;Map position: 13R
C;Function: 13R
C;Function: required for pre-rRNA processing
A;Description: required for pre-rRNA processing
C;Kuperfamily: ribosomal RNA processing protein RRP5
C;Keywords: nucleus; RNA binding
Query Match
Best Local S
Matches 5
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Local Similarity 53.3%;
es 8; Conservative
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Similarity 41.7%;
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     Score 39; DB 2; L. pred. No. 1.1e+02; 5; Mismatches 2;
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RESULT 23

B87407

B87407

RESOLTS 2

RESOLUTION AND ACCESSED AND ACCESSED BENDERS

C; Species: Caulobacter crescentus

C; Species: Caulobacter crescentus

C; Species: Caulobacter crescentus

C; Species: Caulobacter crescentus

C; Species: Caulobacter crescentus

C; Accession: B87407

R; Nierman, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidel

R; Nierman, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.;

B.; Liaub, M.T.; DeBoy, R.T.; Dodson, R.J.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frain, J.; Eisen, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

R; Nierman, M.C.; Frain, J.; Heidel

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R; Nierman, M.C.; Heidel

R; Nierman, M
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R; Favello, T. the EMBL Data Library, June 1994
submitted to the EMBL Data Library, June 1994
submitted to the EMBL Data Cibrary, June 1994
A; Description: The sequence of S. cerevisiae cosmid 9196.
A; Reference number: S46794
A; Accession: S48937
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C;Superfamily: Escherichia coli ribosomal protein L17
hypothetical protein ORF61 - ictalurid herpesvirus 1 (strain auburn 1) C. Species: ictalurid herpesvirus 1 C. Species: ictalurid herpesvirus 1 A. Note: host ictalurus punctatus (channel cattish) C. plate: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999 C. Accession: H36792 R. Davison, A. J. R. Davison, A. J. R. Davison, A. J. Submitted to GenBank, January 1992
                                                                                                                                                                                                                                                                  RESULT 25
H36792
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A; Residues: 1-223 <FAV>
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A;Cross-references: SGD:S0001023; MIPS:YHL031c
A;Map position: 8L
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Best Local S
Matches 5
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Best Local
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565 RVISVNSRGNVH 576
                                                                                                                                                                                                                                                                                                                                                                                                                       152 VDRLISQAWETRSQFHS 168
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5; Conserv
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larity 33.3%;
Conservative
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; Pred. No.
7; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score 38; DB; Pred. No. 18; 2; Mismatches
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aft, D.H.; Ko
C.; Fraser, C
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A;Gene: SGD:YIM1
A;Cross-references: SGD:S0004760
A;Map position: 13R
C;Keywords: transmembrane protein
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Mol. Gen. Genet. 228, 167-176, 1991
A;Title: Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae shows
A;Reference number: S16817; MUID:91360060; PMID:1886606
A;Accession: S16819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Badcock, K.; Churcher, C. submitted to the EMBL Data Library,
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A; Residues: 1-319 <DAV>
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RESULT 27
JE0398
ribosomal protein
                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 196-365 <HUN>
A;Residues: 196-365 <HUN>
A;Cross-references: GB:Z49705; EMBL:Z49700; NID:g825556; PIDN:CAA89788.1; PID:g825557;
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S54510
A; Accession: S54510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-120,'I',122-233,'I',235-279,'N',281-295,'S',297-365 R;Hunt, S.; Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-316 <BAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S50388
A; Accession: S50409
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C;Date: 27-Jan-1995 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YMR152w - yeast (Saccharomyces cerevisiae) N; Alternate names: hypothetical protein YM8520.01; hypothetical
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S50409
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                                                                                                                                                                                                                                                                    F;170-186/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: S50409; S16819; S54510; S54597
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                                                                                                                                            IDRLVSIRTRGQI 13
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53.8%;
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Pred. No. 27;
4; Mismatches
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                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                            Score 38;
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    (strain
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PMID:1727613
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32;
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  A;Molecule type: DNA
A;Residues: 1-142 <KUR>
A;Cross references: GB:AE008917; PIDN:AAL51963.1;
A;Experimental source: strain 16M
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                                                                                 A; Status: preliminary
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, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A; Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wadd, T.; Yamazaki, T.; Kuramitsu, S.; Kyogoku, Y.
J. Biochem. 125, 143-150, 1999
A;Title: Cloning of the RNA polymerase alpha subunit gene from Thermus thermophilus H A;Reference number: JE0397; MUID:99098837; PMID:9880810
A;Accession: JE0398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S77863; S48596
C;Accession: S77863; S48596
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals A;Reference number: S77739; MUID:96059641; PMID:7476192
A;Accession: S77863
                                                                                                                                        LSU ribosomal protein L17P [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C;Accession: AH3349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycoplasma capricolum
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Escherichia coli ribosomal protein
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A; Residues: 1-118 <WAD>
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C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z33050; NID:g541697; PIDN:CAA83721.1; PID:g4379134
A;Experimental source: ATCC 27343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-119 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                     RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribosomal protein L17 - Mycoplasma capricolum (fragment)
N;Alternate names: protein MC060
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;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: JE0398
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PID:g17982722; GSPDB:GN00190

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RESULT 30
TQ11/22
3b.protein - canine coronavirus
C;Specles: canine coronavirus
C;Specles: canine coronavirus
C;Specles: canine coronavirus
C;Specles: canine coronavirus
C;Specles: canine coronavirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: JQ1/22
C;Accession: JQ1/22
A;Fitle: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNP
A;Reference number: PQ0481; MUID:93057357; PMID:1431811
A;Accession: JQ1/22
A;Molecule type: mRNA
A;Residues: 1-251 GHORD
A;Cross-references: DDBJ:D13096
A;Experimental source: strain Insavc-1
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A:Gene: BMEI0782
A:Map postion: I
C:Superfamily: Escherichia coli ribosomal protein L17
Search completed: August 29, 2003, 18:48:28 Job time: 17.4286 secs
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179 LVSIATRGLAHA 190
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48 VEKLVTLGKRGDLHA 62
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Run 8

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Title:
Perfect score:
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1 IDRLVSIRTRGQII
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HSSP; P04063; IAVA.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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J. Mol. Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (CLONE GRAMY56).
Rahmatullah R.J., Huang J.-K., Clark K.L., Reec Chandra G.R., Muthukrishnan S.;
"Nucleotide and predicted amino acid sequences for high-pI alpha-amylases from barley.";
Plant Mol. Biol. 12:119-121(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
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                                                         SEQUENCE
                                                                                                               SIGNAL
                                                                                                                              Calcium;
                                                                                                                                                                                                                                          EMBL; X15227; CAA33299.1;
EMBL; K02636; AAA32932.1;
                                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                           Hydrolase;
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                Local
                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: TYPE B ISOZYME MRNA CELLS AND INCREASES A HUNDRED-FOLD GIBBERELLIC ACID.
SIMILARITY: BELONGS TO FAMILY 13 O KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY. DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM DEVELOPING PLANT EMBRYO.
                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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J.-K., Swegle M., Dandekar A.M., Muthukrishnan
l Similarity
13; Conserv
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86.7%;
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yta; Liliopsida; Poales; Poa
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and 963).
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SEQUENCE FROM N.A.
MEDLINE-85159405; PubMed-6335720;
MEDLINE-85.59405; PubMed-6335720;
Unang J.-K., Swegle M., Dandekar A.M., Muthul
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SEQUENCE
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Triticeae; Hordeum.
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13-AUG-1987 (Rel. 05, Last sequence update)
13-ADG-1988 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clone 103) (Fragment).
                                                                                                                                                                                                                                                                  Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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P04748;
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                                                                                                                                                                                                                                                                                                              InterPro; IPR006047; Alpha_amyl_cat.
                                                                                                                                                                                                                                                                                                                                   PIR; A21826; A21826.
HSSP; P04063; 1AVA.
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BE5233AE1D265F72 CRC64;
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gene family
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RESULT

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EMBL; X15226; CAA33298.1; -
EMBL; X05637; AAA98790.1; -
PIR; A31960; ALBHB.
PDB; 1AMY; 13-MAY-95.
PDB; 1AVA; 16-MAR-99.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase).
AMY1.2.
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Rahmatullah R.J., Huang J.K., Clark K.L., Reeck G.R.,
Chandra G.R., Muthukrishnan S.;
"Nucleotide and predicted amino acid sequences of two different genes
for high-pI alpha-amylases from barley.";
Plant Mol. Biol. 12:119-121(1989).
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P04063;
                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-94254083; PubMed-8196040;
MEDLINE-94254083; PubMed-8196040;
Kadziola A., Abe J.-I., Svensson B., Haser R.;
"Crystal and molecular structure of barley alpha-amylase.";
J., Mol. Biol. 239:104-121(1994).
                                                                                                                                                                                                                                                                                                                                                    aleurone cells.";
J. Biol. Chem. 260:3731-3738(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
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"Two barley alpha-amylase gene families are regulated differently
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Hydrolase; Glycosidase;
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR0060407; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha_amylase; 1.
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13-BUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4-alpha-D-glucan olucanohydrolase) (Clone 168) (Fragment).
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SEQUENCE FROM N.A.
MEDLINE-85159405; PubMed-6335720;
MEDLINE-85159405; PubMed-6335720;
Sweqle M., Dandekar
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                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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Expression and regulation of alpha-amylase gene family
                                                                                                                                                                                                                                                                                                                                                                                                MO1. Appl. Genet. 2:579-588(1984).

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                               AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                      THERE
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73.3%;
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                                                                                                                                                                                                                                                                                                                                    ARE
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                                                                                                                                                                                                                                                                 ISOZYME MRNA
HUNDRED-FOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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Pred. No.
                                                                                                                                                                                                                                                                                                                                    AT LEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                    4 TYPES OF ALPHA-AMYLASE
                                                                                                                                                                                                                                                                 IS UNDETECTABLE IN UNSTIMULATED AFTER STIMULATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
0.011;
                                                                                                                                                                                                                        GLYCOSYL HYDROLASES,
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                                                                                  as its content
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                                                                                                                                                                                                                                                                                                                                                                                FOR USE BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in barley
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                                                                                                                                                                                                                          ALSO
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Ra Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Grandi G.,
Rollseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Rurita K., Ispidins A., Isrdinis S. Tardinis urita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A. Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A. Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A. Moone D., O'Reiliy M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A. Noone D., O'Reiliy M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A. Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A. Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A. Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
A. Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
A. Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
A. Sorokin A., Tacconi E., Takagi T., Takahashi H., Takamaru K.,
A. Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
A. Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
A. Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
A. Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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01-OCT-1996
28-FEB-2003
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MEDLINE-96349105; PubMed=8760912;
Azevedo V., Zumstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the Bacillus subtilis chromosome region the serA and kdg loci cloned in a yeast artificial chromosome. Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006047; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Garbohydrate metabolism;
Calcium; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K02635; AAA32931.1; -. PIR; C21826; C21826. HSSP; P04063; IAVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serror P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDRLVSVSTRHGIHS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDRLVSIRTRGQIHS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 34, Last
. 41, Last
synthase
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34, Last sequence update)
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15140
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73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВY
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947F71F5E13DD2A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 6
AMY1_ORYSA
ID AMY1_O
AC P17654
DT 01-AUG
DT 01-AUG
DT 15-SEP
DE ALPha-
DE Glucan
GN AMY1.1
OS ORYZA
OC Sperma
OC Ehrhai
OC Sperma
OC SPERMA
OC SPERMA
CO NCB1_1
OS SPERMA
OC STRAIL
RN [1]
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R EMBL; Z99115; CAB14122.1; -.

R EMBL; Z99115; CAB14122.1; -.

R EMBL; A69593; A69593.

R PIR; A69593; A69593.

R SUBTLILIS; BG11523; bcsA.

R Interpro; IPR001099; N-C_synthase.

R Pfam; PF00195; Chal_stil_synt; 1.

R Pfam; PF02797; Chal_stil_synt; 1.

R PF02797; Chal_stil_synt; 1.

R PF02797; Chal_stil_synt; 1.

R PF02797; Chal_stil_synt; 1.

R PROSTITE; PS00441; CHALCONE_SYNTH; 1.

R PROSTITE; PS00441; CHALCONE_SYNTH; 1.

TIACT_SITE 144 144

SEQUENCE 365 AA; 40713 MW; 2C6779BD648925A4 CRC64;
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STRAIN-168;
Saxild H.H., Chris
Submitted (JAN-199
-!- CATALYTIC ACT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p17654;
p17654;
p1.40G-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).
AMY1.1 OR AMY1A.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzaa.
MCBI_TaxID=4530;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-GV. Japonica M202;
STRAIN-GV. Japonica M202;
MEDLINE-91346557; pubMed-2102847;
MEDLINE-91346557; pubMed-2102847;
Flant Mol. Stolie Medical Manageria Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical Medical
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SEQUENCE FROM N.A. (CLONE POS103).
STRAIN-CV. Japonica M202;
MEDLINE-90318322; PubMed-2370848;
O'Neill S.D., Kumagai M.H., Majumdi
Rodriguez R.L.;
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Nature 390:249-256(1997).
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66.7%;
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                                          Majumdar
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Gram-positive
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bacterium Bacillus
                                     Sutliff T.D.
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AMY3_HORVU

P04747;

13-AUG-1987 (Rel. 05, Created)

13-AUG-1987 (Rel. 05, Last sequence upda
15-UUL-1999 (Rel. 38, Last annotation up
Alpha-amylase type B isozyme precursor (
glucan glucanohydrolase) (Clone PHV19)

AMY1.3.

Hordeum vulgare (Barley).

Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida
Triticeae; Hordeum.

NCBI_TaxID-4513;

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SEQUENCE
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EMBL; X24286; AAA33885.1; ALT_INIT.
PIR; S10013; S10013.
HSSP; P04063; 1AVA.
Gramene; P17654; --
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SIGNAL
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SMART; SM00642; Aamy; 1.
Hydrolase; Glycosidase;
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyoc_bydro_13.
Pfam; PF00128; alpha-amylase; 1.
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359 IERLVSIRNRQGIH 372
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l Similarity 71.4%;
l0; Conservative
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428 AA;
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zyme precursor (EC 3.2.1.1
(Clone PHV19) (Fragment).
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yta; Liliopsida;
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N-110450 CALCOMACTECGAG CRCG4;
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Pred. No. 0.6;
1; Mismatches
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a; Poales; Po
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aceae; Pooideae;
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30-MAY-2000 (Rel. 39,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clone.
        STRAIN-129/SvJ;
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium;
                               SEQUENCE FROM
                                                                    NCBI_TaxID=10090;
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COEACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY

REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC

ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING

THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME

THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE

DEVELOPING PLANT EMBRYO.

MISCELLANDOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: TYPE
CELLS AND INCREASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Endohydrolysis
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8; Conser
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pean Bioinformatics Institute.
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TISSUE=Liver;
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                                                                                           Chordata;
Rodentia;
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88.9%;
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HUNDRED-FOLD
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Sciurognathi;
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and abscisic acid on alpha-amylase
ayers studies using an alpha amylase
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Best Local S
Matches 7
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30-MAY-2000
30-MAY-2000
16-OCT-2001
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Alberti S., Steffensen K.R., Gustafsson J.
"Structural characterisation of the mouse
genes LXRalpha and LXRbeta.";
Gene 243:93-103(2000).
                                                                                                                                                                                                                                  DOMAIN
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute use by non-profit institutions as 1 modified and this statement is not rem
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                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000536; Hormone InterPro; IPR001723; Stdhrmm InterPro; IPR001628; Znf_C4s Pfam; PF00104; hormone_rec; Pfam; PF00105; Zf_C4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
  Oxysterols
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                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                     SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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MGD; MGI:1352462; Nr1h3.
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pinitted (AIG-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
GENES DEFINED BY LIXES. LIXES ARE DR4-TYPE RESPONSE ELEMENTS
CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLOTIDE HALF-
SITES SPACED BY FOUR NUCLEOTIDES. LRXA PLAYS AN IMPORTANT ROLE IN
THE REGULATION OF CHOLESTEROL HOMEOSTASIS.
SUBCELLULAR LOCATION: Nuclear (Potential).
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfamily.
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AJ132600;
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(Rel. 40, Last annotation updat
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; CAB51923.1;
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                                                                 STANDARD;
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53.8%;
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                                                                                                                                                                                                                                                                        C4-TYPE.
                                                                                                                                                                                                          Score 39;
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R -> P (IN REF. 2).
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notation update) (Nuclear orphan (Liver X receptor alpha)
                                                                 PRT;
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WHOL Cell. Biol. 14:7025-7035(1994),

COLORITON: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM TIS ROLE AS A SILENT DAA-BINDING PARTHER TO AN ACTIVE LIGAND-
BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET GENES DEFINED BY LIXES. LIXES ARE DA4-TYPE RESPONSE ELEMENTS

COLORARCTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANDICLOTIDE HALF-

COLORARCTERIZED BY FOUR NUCLEOTIDES. LIXAA PLAYS AN IMPORTANT ROLE IN THE REGULATION OF CHOLESTEROL HOMEOSTASIS (BY SIMILARITY).

COLORARCTERIZED ST FOUR RUCLEOTIDES. LIXAA PLAYS AN IMPORTANT ROLE IN THE REGULATION OF CHOLESTEROL HOMEOSTASIS (BY SIMILARITY).

COLORARCTERIZED ST FOUR NUCLEOTIDES. LIXAA PLAYS AN IMPORTANT ROLE IN SUBJECT FOR THE REGULATION SHOULD STATE AND THE RESPONSE ELEMENTS. UNITED TO SUBJECT (POTENTIAL).

COLORARCTERIZED STRUCTURE OF LIXAA AND RIXA (BY SIMILARITY).

COLORARCTERIZED STRUCTURE OF LIXAA AND RIXA (BY SIMILARITY).

COLORARCTERIZED STRUCTURE OF LIXAA AND RIXA (BY SIMILARITY).

COLORARCTERIZED STRUCTURE OF LIXAA AND RIXA (BY SIMILARITY).

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PRINTS; PF
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TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content was the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the c
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responsive elements and i
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NR1H3 OR LXRA.
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erPro; IPR001723; Stdhrmn_rece_lig.
erPro; IPR001723; Stdhrmn_receptor.
erPro; IPR001723; Stdhrmn_receptor.
m; PF00104; hormone_rec; 1.
nm; PF00105; zf-C4, 1.
INTS; PR00398; STEDHORNONER.
INTS; PR00398; STEDHORNONER.
INTS; PR00398; STEDHORNONER.
INTS; PR00398; STEDHORNONER.
ART; SM00399; Znf_C4steroid; 1.
ART; SM00430; HOLL; 1.
ROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
eceptor; Transcription regulation; DN:
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ota; Metazoa; Chordata;
ia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR RECEPTOR-TYPE.
(24-TYPE.
C4-TYPE.
C4-TYPE.
LIGAND-BINDING (POTENTIAL).
131A84AB142AEA82 CRC64;
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DNA-binding; Nuclear
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C STRAIN=129/SvJ; TISSUE-Liver;

X MEDLINE=20156373; PubMed=10675617;

A Alberti S., Steffensen K.R., Gustafsson J.-A.;

A Alberti S., Steffensen K.R., Gustafsson J.-A.;

Province of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse nuclear oxysterol process of the mouse oxysterol process of the mouse oxysterol process of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mouse of the mou
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C 060644;
C 060644;
T 30-MAY-2000 (Rel. 39, Created)
T 30-MAY-2000 (Rel. 39, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Oxysterols receptor LXR-beta (Liver x receptor beta) (Nu receptor interacting protein No.15)
E x receptor LXR-beta) (Ubiquitously-expressed nuclear recept x receptor LXR update)
E x receptor LXR bota) (Topical No.15)
Nu NRSH2 OR LXRB OR UNR OR RIP15.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Muz NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SISUE-Liver;
TISSUE-Liver;
MEDLINE-95280959; PubMed-7760852;
Seol W., Choi H.S., Moore D.D.;
"Isolation of proteins that interact spreeptor: two novel orphan receptors.";
Mol. Endocrinol. 9:72-85(1995).
                                                                                                                                                                                                                                                                                   InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; Zf-C4; 1.
PRINTS; PR00348; STROHORMONER.
PRINTS; PR000047; STROHORMONER.
PRINTS; PR000047; ZTROHORMONER.
  Receptor: Tr
Zinc-finger
DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
DOMAIN
SEQUENCE 4
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                                                                                                                                                                                                           probom; PD000035; Znf_C4steroid; 1.
sware; sw00430; HOLI; 1.
sware; sw00399; Znf_C4; 1.
sware; sw00399; Znf_C4; 1.
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EMBL; AJ132602; CAB51924.1; -
PIR; I49021; I49021.
HSSP; P03372; 1HCQ.
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MGD; MGI:1352463; Nr1h2
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     49719
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     MW.
1.
DNA-binding; Nuclear
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nuclear oxysterol receptor
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HALF-SITE
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REQUENCE FROM N.A.

REPLINE-Sprague-Dawley; TISSUE-Vagina;

RC STRAIN-Sprague-Dawley; TISSUE-Vagina;

RX MEDLINE-95062154; pubMed-9971966;

RA Song C., Kokontis J.M., Hiipakka R.A., Liao S.;

RA "Ubiquitous receptor: a receptor that modulates gene activation by retinoic acid and thyroid hormone receptors.";

RI retinoic acid and thyroid hormone receptors.";

RI Proc. Natl. Acad. Sci. U.S.A. 91:10809-10813(1994).

CC -1- FUNCTION: ORDHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRAN CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).

CC STRUINIT: FORMS A HETERODIMER WITH RXR.

CTRUINIT: FORMS A HETERODIMER WITH RXR.
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NRH2_RAT
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Best Local
                                    InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; Zf-C4; 1.
Pfam; PF000195; Zf-C4; 1.
PRINTS; PR00398; STRDHDRMONER.
PRINTS; PR00047; STROIDFINGER.
PRIODOM; PD000035; Znf_C4steroid; 1.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Oxysterols receptor Lix-beta (Liver X receptor beta) (Nuclear orphan receptor Lix-beta) (Ubiquitously-expressed nuclear receptor) (UR)
                                                                                                                                                                                                                                                                                                  between
the Euro
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             SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
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HSSP; P03372; 1HCQ.
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                                                                                                                                                      RANSFAC; T04451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a member of the nuclear receptor superfamily he 9-cis-retinoic acid receptor."; Natl. Acad. Sci. U.S.A. 92:2096-2100(1995).
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PubMed=7892230;
NUCLEAR_RECEPTOR; 1
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Pred. No. 9.1;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pelto-Huikko
                                                                                                                                                                                                                                                                      Usage
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                                                                                                                                                                                                                                                                                                 restrictions
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Halton J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
"Generation will RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHIFTS RXR FROM C. INTERACTION WITH RXR SHI
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Best Local :
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ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013133; 096H87;
30-MAY'2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
0Xysterols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan receptor LXR-alpha).
NR1H3 OR LXRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Willy P.J., Umesono K., Mangelsdorf D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95262897; PubMed=7744246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLVSIRTRGQIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:1033-1045(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor that
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98
140
446
168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND-BINDING (POT)
POLY-GLN.
POLY-PRO.
G -> V (IN REF. 2).
MISSING (IN REF. 2).
A -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ψ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13DF6DC2F0F5FA4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.M., Heyman R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG
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RESULT 13

NRH2_HUMAN

ID NRH2_H

AC P55055

DT 01-OCT

DT 01-OCT
                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
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EMBL; BC008819; AAHUUV
PIR; I38975; 138975;
HSSP; P03372; 1HCQ.
TO2752; T02752;
TO2764; NR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005713; F:transcription co-activa
GO; GO:0003713; F:transcription co-activa
InterPro; IPR00336; Hormone_rec_lig;
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
pfam; pF00104; hormone_rec; 1.
pfam; pF00105; Zf-C4; 1.
pfam; pF00105; Zf-C4; 1.
pfam; pF00105; Zf-C4; 1.
prINTS; PR00347; STROIDFINGER.
PRINTS; PR00347; STROIDFINGER.
PRINTS; PR00303; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00430; MOLL; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-1
NRH2_HUMAN
P55055; Q12970;
O1-OCT-1996 (Re
O1-OCT-1996 (Re
                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
ZN_FING
ZN_FING
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note-No experimental confirmation available:
-ITISSUE SPECIFICITY: VISCERAL ORGANS SPECIFIC EXPRESSION. STRONG
EXPRESSION WAS FOUND IN LIVER, KIDNEY AND INTESTINE FOLLOWED BY
SPLEEN AND TO A LESSER EXTENT THE ADRENALS.
-I- INDUCTION: BY 9-CIS RETINOIC ACID (9CRA).
-I- SINULTARITY: Belongs to the nuclear hormone receptor family. NR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +++
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                             CONFLICT
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SITES SPACED BY FOUR NUCLECTIDES. LIXA PLAYS AN IMPORTANT ROLE IN
THE REGULATION OF CHOLESTEROL HOWEDSTASIS.
SUBUNIT: HETERODIMER OF LXRA AND RXR.
SUBCURIT LECTRODIMER OF LXRA AND RXR.
SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1;
IsoId=Q13133-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-2;
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                                                                                                                                                             410
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                                                                                                                                                                                                                                     Similarity 53.77; Conservative
                                                                                                                                                          KLVSLRTLSSVHS
                                                                                                                                                                                  RLVSIRTRGQIHS
                                                                                                                                                                                                                                                                                                                       196
447 /
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98 118
134 158
134 158
215 434
237 296
(Rel.
                                                                                                                                                                                                                                                                                                                       8
                                                          STANDARD;
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50395
                                                                                                                                                                                                                                                          53.4%;
Created)
Last sequ
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                                                                                                                                                                                                15
                                                                                                                                                             422
                                                                                                                                                                                                                                                                                                                       WW.
                                                                                                                                                                                                                                     ; Score 39; DB 1; Pred. No. 9.1; 3; Mismatches
  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR I
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                      Missing (in isoft /FTId=VSP_003664 A -> R (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                   LIGAND-BINDING
                                                          PRT;
                                                                                                                                                                                                                                                                                                                     -> R (IN REF. 1).
0D27B237440F8C9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           co-activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR-TYPE
                                                          461
                                                                                                                                                                                                                                                                             DB 1; Length 447
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                                                                                                                                                                                                                                                                                                                                                                                isoform
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EMBL; U07132; AAA61783.1; -. EMBL; BC007790; AAH07790.1; -. EMBL; U14534; AAA58594.1; -. PIR; JC4014; JC4014.

for

.ch/announce/

TRANSFAC;

ANSFAC; T04453; -. Tew; HGNC:7965; NR1H2. 1600380; -.

C:nucleus;

\(\frac{1}{2}\) \(\frac{1}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \

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RX KEDLINE-2338857; PubMed-12477932;
RX MEDLINE-2338857; PubMed-12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Welellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
RA Piakes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Butterfield V.S.N., Krzyvinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences .,
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 7-461 FROM N.A.

SONG C., KONKONTIS J.M., Hilpakka R.A., Liao S.;

SONG C., KONKONTIS J.M., Hilpakka R.A., Liao S.;

T "Ubiquittous receptor: a novel receptor that modulates ger

by retinoic acid and thyroid hormone receptors.";

SUBMITTED CORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DO

COLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS I

C SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).

C -1 SUBUNIT: FORMS A HETERODIMER WITH RXR.

C -1 SUBCELLULAR LOCATION: Nuclear (Potential).

C -1 SIMILARITY: Belongs to the nuclear hormone receptor i
                                                                                                                                                                                            This SWISS-PRO7 entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95011628; PubMed-7926814; Vogel R., Shinar D.M., Endo N., RutLedge S.J., Vogel R., "NER, a new member of the gene family encoding hormone nuclear receptor."; Gene 147:273-276(1994).
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Oxysterols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (Nuclear receptor NER).
NR1H2 OR LXRB OR UNR OR NER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           Ubiquitous.
to the nuclear hormone receptor family.
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ZN_FING
ZN_FING
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SMART; SM00430; HOLI; 1.
SMART; SM000399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                                                                                                  Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Niegemann E., Schenk-Groeninger R., Servos J., Wehner E., Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duest Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., F Siegers K., Baur A., Boles E., Miosga T., Schaaff-Gerstenschlæger I., Zimmermann F.K.; Schaaff-Gerstenschlæger I., Zimmermann F.K.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                               STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-CCT-1994 (Rel. 30, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 67.6 kDa protein in CDC28-ARL1 intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P38289;
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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                                                                           SEQUENCE
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                                                                                       Hypothetical
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$0000367; DEM1.
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                         Similarity
8; Conser
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 IDRLVSIRTRGQIHS
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IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
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                          Conservative
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Schenk-Groeninger R., Servos J., Wehner E.,
endel M., Bauer J., Braun H., Dern K., Duest
Hedges D., Kiesau P., Korol S., Krems B., P
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Pred. No. 9.4;
3; Mismatches
                                     Score 39;
Pred. No.
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                          Mismatches
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EMBO J. 15:5701-5714(1996).
-i- FUNCTION: INVOLVED IN THE BIOGENESIS OF RRNA.
-i- FORMATION OF 18S AND 5.8S RRNA.
-i- SUBCELIULAR LOCATION: Nuclear; nucleolar.
-i- SIMILARITY: Contains 4 HAT repeats.
-i- SIMILARITY: Contains 11 S1 motif domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PubMed=9169872;
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01-NOV-1997
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                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                       EMBL; Z49939; CAA90200.1; PIR; S57596; S57596.
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MEDLINE=97051828; PubMed=8896463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The nucleotide sequence
                                                                                                                                         PROSITE; PS50126; S1; 11
                                                                                                                                                                                                                                                             HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                 ; P05055; 1SRO.
S0004842; RRP5
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                                                                                                                               processing;
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20s pre-rRNA; IPI
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les S., Han
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RESULT 16
YHD1_Y
YHD1_Y
AC P38736
DT 01-FEB
DE Hypoth
GN YHL031
OS Saccha
OC ENKALY
OC NCBL_T
RN [1]
RR SEQUEN
RA LACTER
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RESULT 17
VG61_HSVI1
ID VG61_HSVI1
AC Q00122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hiller L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser
Nhan M., Rifkin L., Stepeter H., Trevaskis E., Vaughan K
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
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PIR; S48937; S48937.
SGD; S0001023; GOS1.
GO; GO:0016021; C:integral to membrane;
Pfam; PP05008; V-SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of Saccharomyces cerevisiae VIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288c / AB972;
MEDLINE-94378003; Pub
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YHL031C
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P38736;
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223 AA; 25394 MW;
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Pred. No.
                           PRT;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91360060; PubMed-1886606;
Behrens M., Michaells G., Pratje E.;
Behrens M., Michaells G., Pratje E.;
"Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae shows sequence similarity to the Escherichia coli leader peptidase.";
Shows sequence similarity to the Escherichia coli leader peptidase.";
Can. Genet. 228:167-176(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 01-DEC-1992 (Rel. 01-DEC-1992 (Rel. Hypothetical gene 61.
                                                      PubMed=9169872;

PubMed=9169872;

Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ictalurid herpesvirus 1 (Channe Viruses; dsDNA viruses, no RNA Ictalurid Herpes-like viruses. NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                          YM07_YEAST STANDARD; PRT; 365 AA.
P28675;
01-DEC-1992 (Rel. 24, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 41.6 kDa protein in IMP1-HLJ1 intergenic region (RF1095).
YMR152W OR YM9375.22 OR YM8520.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Channel catfish virus: a new type of herpesvirus. Virology 186:9-14(1992).
                            Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M75136; AAA88164.1; -. PIR; H36792; H36792. Hypothetical protein. SEQUENCE 319 AA; 36909 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 VDRLGKLRARGEV 225
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no RNA stage;
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Lage; Herpesviridae;
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Matches 7
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STRAIN-HBB / ATCC 27634;
MEDLINE-9909837; PubMed-9880810;
Wada T., Yamazaki T., Kuramitsu S., Kyogoku Y.;
"Cloning of the RNA polymerase alpha subunit gene from Cloning of the RNA polymerase alpha subunit gene from Cloning of the RNA polymerase alpha subunit gene from Cloning of the RNA polymerase alpha subunit gene from Cloning of the Protein.";
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SGD;
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                                                                                                                                                                                                                                                                                                                                                    thermophilus HB8 and characterization of the protein.";
J. Biochem. 125:143-150(1999).
-i- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Z9H5;
30-MAY-2000
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                                                                                     EMBL; AB024328; BAA75550.1; -. PDB; 1GD8; 28-JAN-03. InterPro; IPR000456; Ribosomal_L17.
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
50s ribosomal protein L17.
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             ProDom; PD004277; Ribosomal_L17; 1.
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                                                                  Pfam; PF01196;
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; $0004760; YIMI.
; $0004760; YIMI.
; $00005811; C:lipid particle; IDA.
; $0:0005743; C:mitochondrial inner membrane;
; $0:0008233; F:peptidase activity; IMP.
; $0:0006627; P:mitochondrial processing; IMP.
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SEQUENCE
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InterPro; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17; 1.
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Bork P., Ouzounis C., Casari G.,
Gilbert W., Gillevet P.M.;
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SEQUENCE 118 AA;
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STRAIN=ATCC 27343 / Kid;
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                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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759; L17; 1.
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13715 MW; C9B8DD552F6C42AF CRC64;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
50S ribosomal protein L17.
RPLQ OR R01381 OR SMC01283.

update)

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RESULT 22
VNS3_CVCAI
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AC P36695;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Nonstructural protein 3-B (ORF 3B).
Canine enteric coronavirus (strain Insavc-1) (CCOV) (CCV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Nid
COronaviridae; Coronavirus.
NCBI_TaxID-36391;
This
                                                                 SEQUENCE FROM N.A.

MEDLINE-93057357; behomed-1431811;

MEDLINE-93057357; behomed-1431811;

Horsburgh B.C., Brierley I., Brown T.D.K.;

Horsburgh B.C., Brierley I., Brown T.D.K.;

"Analysis of a 9.6 kb sequence from the 3' end of canine corona

"Analysis of a 9.6 kb sequence from the 3' end of canine corona

"Gen. Virol. 73:2849-2862(1992).

"I. SIMILARITY: Belongs to the coronavirus NS3b protein family.
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EMBL; AL591787; CAC45960.1; -.
INTERFOO 1: FR000456; Ribosomal_L17.
IPfam; PP01196; Ribosomal_L17; 1.
ProDom; PP004277; Ribosomal_L17; 1.
TIGREAMS; TIGR00059; L17; 1.
PROSITE; PS01167; CAMPLETE proteome.
RIBOSOMAL_L17; 1.
RIBOSOMAL Protein: Complete proteome.
RIBOSOMAL_L17; 1.
RIBOSOMAL PROTEIN: COMPLETE PROTEOME.
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Bolstard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Gallbert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A., 98:9877-9882(2001).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiacee; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID-382;
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-Hubler F., Gouzy
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through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nidovirales;
                                                                                                                                                                                               coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT
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Best 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                       HSSP; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0924X0;
0924X0;
09-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Indole-3-glycerol phosphate synthase 2 (EC 4.1.1.48) (IGPS TRPC2 OR SCO3211 OR SCE8.04C.
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no results by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete coelicolor A3(2),";
Nature 417:141-147(2002).
-i- FUNCTION: THE FUNCTION OF THE SECOND TRP OPERON
TO PRODUCE TRP FOR THE BIOSYNTHESIS OF CALCIUM-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                            EMBL; AL035654; CAB38582.1;
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SEQUENCE 250 AA; 28426 MW; FCB7ABFD83DD9CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRC2_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D13096; BAA02411.1; ALT_TERM.
InterPro; IPR004293; Corona_NS3b.
Pfam; PF03053; Corona_NS3b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                   send an
                                                                                                                                                                             FUNCTION: THE FUNCTION OF THE SECOND TRP OPERON IN S.COELICOLOR TO PRODUCE TRP FOR THE BIOSYNTHESIS OF CALCIUM-DEPENDENT ANTIBLOTIC (CDA).

CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose phosphate = 1 (indol-3-yl)91/cerol 3-phosphate + CO(2) + H(2)0.

PATHMAX: Tryptophan biosynthesis; fourth step.

SIMILARITY: BELONGS TO THE TRPC FAMILY.
                                               T36303; T36303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
                    P00909; 1F; MF_00134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LVSIRTRGQIHS 15
                                                                                  requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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                                   1PII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycetaceae;
FMN_enzyme
IGPS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
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Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces.
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12;
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RESULT 24
T4HR_MAGGR
T4HR_MAGGR
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Sep-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tryptophan biosynthesis; Lyase; Decarboxylase; Antibiotic biosynthesis; Complete proteome. SEQUENCE 258 AA; 26815 MW; B2A31BF4B5C6428A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00218; IGPS; 1.
ProDom; PD001511; IGPS; 1.
PROSITE; PS00614; IGPS; 1.
                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                    NADPH and an active-site inhibitor.";
Structure 4:1161-1170(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94155906; PubMed-8112349;
Vidal-Cros A., Viviani F., Labesse G., Boccara M., Gaudry M.;
"Polyhydroxynaphthalene reductase involved in melanin biosynthesis
Magnaporthe grisea. Purification, cDNA cloning and sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., STRAIN-GUYANE 11;
                                                           PIR;
PDB;
                                                                                                                                         entities
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                                                                                                                                                                                           the
                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersson A., Jordan D., Schneider G., Lindqvist Y., 
"Crystal structure of the ternary complex of 
1,3,8-trihydroxynaphthalene reductase from Magnaport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=4091-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sordariomycetes in
NCBI_TaxID=148305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97094973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                       Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
           S41412; S41412.
1YBV; 15-OCT-97.
1DOH; 06-JUN-01.
1GON; 06-JUN-01.
1GOO; 06-JUN-01.
                                                                                                                                                                                                                                                                    SUBUNIT: Homotetramer.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                       tetrahydroxynaphthalene + NADPH. PATHWAY: Fungal melanin biosynthesis.
                                                                                                                                                                                                                                                                                                                                      WHICH ARE USED TO PREVENT BLAST DISEASE IN RICE PLANTS. CATALYTIC ACTIVITY: Scytalone + NADP(+) = 1,3,6,8-
                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CATALXZES THE NADPH-DEPENDENT REDUCTION OF 1,3,6,8-TETRAHYDROXYNAPHTHALENE (T4HN) INTO (+)-SCYTALONE AND 1,3,8-TRIHYDROXYNAPHTHALENE INTO (-)-VERMELONE. THIS ENZYME IS THE BIOCHEMICAL TARGET OF SEVERAL COMMERCIALLY IMPORTANT FUNGICIDES
                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                           L22309;
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                                                                                            AAA19514.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219:985-992(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-8939741;
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ADH_short
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Pred.
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No.
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RESULT 25
ISPE_CORGL
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RRR RN OCC GREET DITC
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00106; a PRINTS; PR00080;
                      Corynebacterineae; NCBI_TaxID=1718;
                                  Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
                                                                                                                                                                                                                                                                               STRAND
     SEQUENCE FROM
STRAIN=ATCC 1:
                                             (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                 Q8NRY0;
                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                          HELIX
                                                                                       SPE_CORGL
                                                                                                                     131 DRVFTINTRGQ
                                                                                                                                N
                                                                                                                                            Similarity 7; Conserv
                                                                                                                           DRLVSIRTRGQ
s.;
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                adh_short;
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                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                   SDRFAMILY.; ADH_SHORT;
                                                                                                                                                                         Corynebacteriaceae;
      DSM
                                                                                                                                                                    29922
                                                                                                                                12
                                                                                                                                                   50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                              Melanin biosynthesis; 3D-structure
                                                                                                                                                  . 68
     20300
                                                                                                                                                                    MW;
                                                                                                                                            Score 37; DB Pred. No. 13; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   NADP (BY SIMILARITY)
      / NCIB 10025
                                                                                                                                                                   2520709137763087 CRC64;
                                                                                        311
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                                                    e (EC 2.7.)
ol kinase)
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Query Match
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Matches
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Ovis aries (Sheep).
Ovis aries (Sheep).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Caprinae; Ov
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005276; BAB98304.1; -.
HAMAP; MF_00061; -; 1.
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR004244; ISPE.
Pfam; PF00286; GHMP_kinases; 1.
TIGRRAMS; TIGR00154, iSpE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             step.
-i- SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
NP_BIND 105
MEDLINE-8132062; PubMed-8264908;
Fisher W.K., Thompson E.O.P.;
Fisher W.K., Thompson E.O.P.;

"Amino acid sequence studies on sheep liver fructose-bisphosphatase
I. The S-peptide.";
Aust. J. Biol. Sci. 33:665-674(1980).
-1- CATALYTIC ACTIVYTY: D-fructose 1,6-bisphosphate + H(2)O = D-
fructose 6-phosphate + phosphate.
-1- ENZYME REGULATION: INHISTED BY AMP, WHICH AFFECTS THE TURNOVER
OF BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last anotation update)
Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphatase)
1-phosphohydrolase) (FBPase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F16P_SHEEP
P09199;
                                                                                                                                                                                     MEDLINE-84079343; PubMed-6316885;
Fisher W.K., Thompson E.O.P.;
Fisher acid sequence studies on sheep
"Amino acid sequence studies on sheep
II. The complete sequence.";
Aust. J. Biol. Sci. 36:235-250(1983).
                                                                                                                                      SEQUENCE OF 1-60.
MEDLINE-81232062;
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                            Ovis.
                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.7%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32630 MW;
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Pred. No.
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; 392FD92100D040F8 CRC64;
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Best Local :
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-! SUBUNIT: HOMOTETRAMER. WITH FOUR BINDING SITES
- EACH FOR THE SUBSTRATE, FOR AMP, AND FOR DIVALENT METAL CATION
(THE GREATEST AFFINITY IS FOR ZINC).
-!- SIMILARITY: BELONGS TO THE FBPASE FAMILY.
PIR, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A05318, A0531
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900636;

21-UTI-1986 (Rel. 01, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-proctose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate)
1-phosphohydrolase) (FBPase).

EBP1 OR EBP.
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MEDLINE-83117639; PubMed-6296821;
Marcus F., Edelstein I., Reardon I., Heinrikson F.
Marcus F., Edelstein I., Reardon pig kidney
fructose-1, 6-bisphosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 79:7161-7165(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92212971; PubMed=1313579; Williams M.K., Kantrowitz E.R.; "Isolation and sequence analysis of the cDNA for pig kidney fructose 1,6-bisphosphatase." Proc. Natl. Acad. Sci. U.S.A. 89:3080-3082(1992).
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Eukaryota; Metazoa;
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                                                                                                                                                                 TISSUE-Kidney:
MEDLINE-8047209; PubMed-6291465;
MCGGregor J.S., Hannappel E., Xu G.-J., Pont
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MCGREGOR J.S. primary structure at the if
Conservation of primary structure at the if
of fructose 1,6-bisphosphatases.",
Arch. Biochem. Biophys. 217:652-664(1982).
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                                                                  SUBSTRATE-BINDING SITE, LIGANDS, MEDLINE=82132308; PubMed=6277165;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-23 AND 43-60.
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                                     Benkovic
Menkovic S.J., Demaine M.M.;
Mechanism of action of fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
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7; Conserv
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46.7%;
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Pred. No.
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ALLOSTERIC REGULATION BY PHOSPHORYLATION (BY PKA).

BY SIMILARITY.
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            1,6-bisphosphatase.";
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                                                                                                                    REVIEW
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X-RAY (KLUSTANDER): PubMed=2154070, MEDLINE=90319088; PubMed=2154070, KE H.M., Zhang Y.P., Lipscomb W.N.; KE H.M., Zhang Y.P., Lipscomb W.N.; "Crystal structure of fructose-1,6-bisphosphatase complexed with fructose 6-phosphate, AMP, and magnesium."; fructose 6-phosphate, AMP, and magnesium."; Natl. Acad. Sci. U.S.A. 87:5243-5247(1990).
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PIR;
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Ke H.M., Zhang Y.P., Liang J.-Y., Lipscomb W.N.;
"Crystal Structure of the neutral form of fructose-1,6-bisphosphatase
complexed with the product fructose 6-phosphate at 2.1-A
resolution.";
                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 39:8565-8574(2000).
-I- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98376425; PubMed=9708979;
Choe J.Y., Poland B.W., Fromm H.J., Honzatko R.B.;
"Role of a dynamic loop in cation activation and allosteric regulation of recombinant porcine fructose-1,6-bisphosphatase.";
Biochemistry 37:11441-11450(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liang J.-Y., Huang S., Zhang Y.P., Ke H.M., Lipscomb W.N.; "Crystal structure of the neutral form of fructose 1,6-bisphosphatase complexed with regulatory inhibitor fructose 2,6-bisphosphate at 2.6-A resolution.";
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Ke H.M., Thorpe C.M., Seaton B.A., Lipscomb W.N., Mar
"Structure refinement of fructose-1,6-bisphosphatase
2,6-bisphosphate complex at 2.8-A resolution.";
J. Mol. Biol. 212:513-539(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad.
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Liang J.-Y., Huang
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                                                                                                                                                                                                                                fructose 6-phosphate + phosphate.

ENAYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER
BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.

PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.

SUBUNIT: HOMOTETRAMER. WITH FOUR BINDING SITES
BACH FOR THE SUBSTRATE, FOR AMP, AND FOR DIVALENT METAL CATION

(THE GREATEST AFFINITY IS FOR INC).

MISCELLANEOUS: THE MOLECULE HAS A HIGHLY REACTIVE CYSTEINE RES:

(CYS-116 OR CYS-128), WHICH TENDS TO FORM MIXED DISCUFIDES (E.C.)

WITH HOMOCYSTINE) BUT IS NOT ESSENTIAL FOR ENZYME ACTIVITY.
L; M86347; AAA31035.1; S37696; PAPGF.; IFBP; 15-APR-92.; 2FBP; 15-APR-92.; 3FBP; 15-APR-92.; 4FBP; 15-JUL-92.; 5FBP; 15-JUL-92.
                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE FBPASE FAMILY.
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  PDB; L. InterPro; L. Team; PF00316; PF0037
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INIT_MET 0
MOD_RES 141
MOD_RES 207
ACT_SITE 274
CONFLICT 27
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ProDom; PD001491; In_FB_phphtase; 1.
PROSITE; PS00124; FBPASE; 1.
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28-MAY-99.
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30-NOV-94.
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  Allosteric enzyme;
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Matches 7
     TISSUE-LIVEY,

MEDLINE-8123840; PubMed-6305949;

Rittenhouse J., Chatterjee T., Marcus F., Reardon I., Heinrikson I Rittenhouse J., Chatterjee T., Marcus F., Reardon I., Heinrikson I Ranno acid sequence of the COOH-terminal region of fructose-1,6-bisphosphatases in relation to cyclic AMP-dependent phosphorylation.

J. Biol. Chem. 258:7648-7652(1983).

-I- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H(2)0 = D-fructose 6-phosphate + phosphate.

-I- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOV.
                                                                                                                                                                                                                                                                                                                          MEDLINE-8904(197; PubMed-2847161; MEDLINE-8904(197; PubMed-2847161; El-Maghrabi M.R., Pilkis J., Marker A.J., Colosia A.D., Fraser B.A., Pilkis S.J.; "cDNA sequence of rat liver fructose-1,6-bisphosphatase for down-regulation of its mRNA by insulin."; Proc. Natl. Acad. Sci. U.S.A. 85:8430-8434(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p19112; 064594;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
1-phosphohydrolase) (FBPase).
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=91115820; pubmed=1846613;
El-Maghrabi M.R., Lange A.J., Kummel
"The rat fructose-1,6-bisphosphatase
of expression.";
J. Biol. Chem. 266:2115-2120(1991).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-96078844; PubMed-7589895;

METCOLOTT: Armbruster L., Okayama H.;

Bertcolott: R., Armbruster L., Okayama H.;

"Liver fructose-1,6-bisphosphatase cDNA: trans-complementation fission yeast and characterization of two human transcripts.";

pifferentiation 59:51-60(1995).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Similarity 46.
7; Conservative
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AMP, WHICH AFFECTS THE TURNOVER
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EMBL; M6240; AAA6625.1; -.
EMBL; M57284; AAA41131.1; JOIN
EMBL; M57279; AAA41131.1; JOIN
EMBL; M57279; AAA41131.1; JOIN
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EMBL; M57282; AAA41131.1; JOIN
EMBL; M57281; AAA41131.1; JOIN
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L_ORYSA
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P27940;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-amylase isozyme C precursor (EC 3.2.1.1)
plucanohydrolase) (Isozyme 1B).
AMYC OR AMY1B.
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SEQUENCE
                                                                 SEQUENCE FROM N.A.
STRAIN-cv. Indica-IR26; TISSUE-Leaf;
MEDLINE-92119260; PubMed-1731997;
Kim J.-K., Wu R.;
"Nucleotide sequence of a high-pI rice
Plant Mol. Biol. 18:399-402(1992).
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                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Es
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoldeae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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PRINTS; PR00377; INFBPHPHTASE.
ProDom; PD001491; In_FB_phphtase; 1.
PROSITE; PS00124; FBPASE; 1.
Hydrolase; Carbohydrate metabolism; Gluconeogenesis;
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SIMILARITY: BELONGS TO THE FBPASE FAMILY.
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S; PR00377; INFBPHPHTASE.
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                                                                                              -amylase
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YM28_YEAST
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Matches 9
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Q03790;
                                                                                                                                                  Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 52.6 kDa protein in IMP1-HLJ1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amylase genes.";
Nucleic Acids Res. 18:70
-!- FUNCTION: IMPORTANT
                                                                               "The nucleotide sequence XIII.";
                                                                                                                                                                                                                                                                                                         STRAIN=S288c / AB972;
PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; P27940;
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Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales;
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TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNOWN AS THE ALPHA-AMYLASE FAMILY.

CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
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S19142; ALRZOC.
; P04063; IAVA.
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43254 MW;
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                                                                                                               of Saccharomyces
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                                                                                                               S., Barrell B.G.; cerevisiae chromosome
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                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                        EMBL;
                                                                                                                  Hypothetical SEQUENCE 47
                                                                                                                                              SGD; S0004762; NUP53.
GO; GO:00005643; C:nuclear pore; IDA.
GO; GO:0000059; P:protein-nucleus import, docking; IPI.
Pfam; PF05172; MPPN; 1.
                                                                                                                                                                                                           ; Z49705; CAA89789.1; -. S54511; S54511.
426 RSLFLRNRGKIHS
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475 AA; 52618 MW;
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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Q40016; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Knox C.A.P., Sonthayanon B.
"Structure and organization
barley.":
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                                                                                      NCBI_TaxID=4513;
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      STRAIN-Himalaya,
                              SEQUENCE FROM N.A
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Q9A8SH7
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O9jmz0 listeria mo
O9jmy9 listeria mo
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Q9vw38 drosophila
Q8syu7 drosophila
Q9a931 caulobacter
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Q9Z717;
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      (TrEMBLrel.
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Created)

PRT;

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SEQUENCE FROM N.A.

Muthukrishnan S.;

Submitted (JUI-1988) to the
EMBL; M17126; AAA32925.1; -
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA levels from individual members of the two different families expressed in aleurone cells.";

J. Biol. Chem. 263:18953-18960(1988).

EMBL; J04202; AAA98615.1;

HSSP: p04063; 1AVA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR00646; Glyco_hydro_13.
Pfam; PP00118; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation updat)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat)
Barley (H.vulgare) alpha-amylase 1.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Triticeae; Hordeum.
                                                                                                                                                        InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SEQUENCE 427 AA; 47402 MW; D21BA
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SIGNAL 1 25 PO
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13; Conserv
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11; Conservative
                     IDRLVSIRTRGQIHS 15
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IDRLVSVRTRHGIHN 372
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427 AA;
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73.3%;
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yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                          Score 54; DB Pred. No. 0.11
2; Mismatches
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alpha-amylase g
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OBLIQGE;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence up
O1-MAR-2003 (TrEMBLrel. 23, Last annotation
Alpha-amylase precursor (EC 3.2.1.1).
Musa acuminata (Banana).
Eukaryota; Viridiplanties; Streptophyta; Embr
Spermatophyta; Magnollophyta; Lillopsida; Zi
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bt
Linher K., Meidman J., Khouri H., Craven B., Bowman C., Dodsor
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzbe
Elsen J., Fraser C.M.;
"Genome sequences of Chiamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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MEDLINE=20330349; PubMed=10871362;
Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiral M., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWL029 from USA.";
ucleic Acids Res. 28:2311-2314(2000).
EMBL; AE001669; AAD19027.1; -.
EMBL; AE002255; AAF38757.1; -.
EMBL; AP002558; BAA939097.1; -.
EMBL; AP002558; BAA93097.1; -.
EMBL; AP002558; BAA93097.1; -.
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Vieira A. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 458 AA;
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                                                    SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=4641;
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InterPro; IPR004558; HemN.
SMART; SM00729; Elp3; 1.
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3; Mismatches 3
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Chlamydiaceae; Chlamydophila.
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a; Zingiberales; Musaceae;
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RV Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;

RV Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;

RY "Sequencing and molecular characterization of a banana alpha-amylase recommended to the fruit ripening";

RU Submitted (JUI-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; AF533648; AAN01149.1;

REMBL; AF533648; AAN01149.1;

REMBL; AF533648; AAN01149.1;

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Matches 7
0974R6 PRELIMINARY;
0974R6;
0974R6;
01-DEC-2001 (TrEMBLrel. 19, C:
01-DEC-2001 (TrEMBLrel. 19, Li
01-MAR-2003 (TrEMBLrel. 23, Li
Hypothetical protein ST0594.
ST0594.
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OBAVBO;
Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Plasminogen precursor (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei, Ostariophysi; Cypriniforme
Cyprinidae; Danio.

OCBI_TaxID-7955;
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SEQUENCE FROM N.A.

Hanumanthaiah R., Day K., Jagadeeswaran P.;

"Comprehensive analysis of blood coagulation pathways in Evolution of coagulation factor genes and identification factor VIII.";

factor VIII.";

Blood Cells Mol. Dis. 0:0-0(2002).

EMBL; AF515276; AAN71006.1; -.
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Sao Paulo, Brasil.
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C STRAIN-ATCC 19089 / CB15;

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Q1-JUN-2001
Q1-JUN-2001
Q1-MAR-2002
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EMBL; AP000983; BAB65591.1; ... InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 544 AA; 62057 MW; 579F2A4E7313ACDA
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Archaea; Crenarchaeota;
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M., Kato Y.,
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InterPro; IPR000072; PD_g
Pfam; PF00431; CUB; 1.
Pfam; PF00341; PDGF; 1.
SMART; SM00042; CUB; 1.
SMART; SM00041; PDGF; 1.
MEDLINE=20317014; PubMed=10858496; Hamada T., U1-Tei K., Miyata Y.; "A novel gene derived from developing member of the PDGF/VEGF family."; FEBS Lett. 475:97-102(2000).
                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2030 (TrEMBLrel. 23, Last annotation update)
101-MAR-2030 (TrEMBLrel. 23, Last annotation update)
Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
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Li X., Ponten A., Aase K., Karlsson
Backstrom G., Hellstrom M., Bostrom
Betsholtz C., Heldin C.-H., Alitalo
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                                                                          TISSUE=Brain;
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HSCDGF OR PDGFC
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Nat. Cell Biol.
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Mammalia; Eutheria;
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, Li H., Soriano F
, Ostman A., Eriks
gand for the PDGF
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D 01-0CT-2001 (TrEMBLrel. 18, Created)

DT 01-0CT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Acetyl-CoA synthetase (Acetate-CoA ligase) (acsA-9) (EC 6.2 ACSA-9 OR SSO2863.

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolo
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RC STRAIN-ARCC 35092 / DSW 1617 / P2;

RX MEDLINE-21332296; pubMed=11427726;

RX She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA She Q., Singh R.K., Confalonieri C., Clausen I.G., Curtis B.A.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Charlebois R.L., Boolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon Sulfolobus solfatarious P2.";

RRA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

BR InterPro; IPR000873; AMP-bind.

DR PAGSITE; PR00154; AMP-BINDING; 1.

DR PRINTS; PR00154; AMP-BINDING; 1.

DR PRINTS; Complete proteome.

SEQUENCE 666 AA; 75799 MW; E2779A7118B7C2C5 CRC64;
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InterPro; IPRO00572; PD_growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00431; CUB; 1.
R SMART; SM00042; CUB; 1.
R SMART; SM00141; PDGF; 1.
R PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01278; PDGF_2; 1.
DR PROSITE; PS0278; PDGF_2; 1.
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Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,

Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,

Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,

Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;

"Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That

Binds to PDGF alpha and beta Receptor ";

J. Biol. Chem. 276:27406-27414(2001).

-I. SIMILARITY: COWTAINS I CUB DOMAIN.

EMBL; AP09143; AAF00049.1;

EMBL; AP09133; AAF00049.1;

EMBL; AP09133; AAF00049.1;

EMBL, AP50718; AAK51337.1;

EMBL, AP50718; AAK51337.1;

EMBL, AP50718; CUB_domain.
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19
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                                                                  Similarity 60. 9; Conservative
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6; Conserv
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LNRLVSITTYKEIHS
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                                                                                 57.5%;
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33
                                                                  Score 42; DB Pred. No. 32; 3; Mismatches
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                                                                               DB 17; Length 666; 32;
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RESULT 12

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DO ORKDC

DO ORKDC

DO OLO

DO OLO

DO OLO

COLO

OC DO OLO

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DT 01-MA
GN RPLQ
GN RPLQ
GN AGTOD
OC Bacte
CC Rhizo
OC NCBI
RN [1]
RN [1]
RN SEQUE
RY MEDLI
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RESTAINTLE / ARCC 49652 / DSM 12025;

CSTRAINTLE / ARCC 49652 / DSM 12025;

X MEDLINE-2103665; PubMed=12093901;

A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Holte J., Unayam L.A., Mason T., Brenner M., Shea T.P., Parkeey D.,

A Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parkeey D.,

A Holt I., Unayam L.A., Mason T., Gruber T.M., Ketchum K.A.,

A Holt I., White O., Gruber T.M., Ketchum K.A.,

A Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

A Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium tepidum TLS, a

Photosynthetic, anaerobic, green-sulfur bacterium.";

BRE TIGR; CT1130;

THEROFOTTON DIFFAR
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Q8KDC4;
Q1-OCT-2002
Q1-OCT-2002
Q1-MAR-2003
                            SEQUENCE FROM N.A.

MEDLINE-21608550; PubMed-11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Mond G.E., Almedda N.F. JT., Woo L.

Chura V.K., Zhou Y., Chen L., Wood G.E., Almedda N.F. JT., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage, G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Rutyavin T., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan I

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                    OBUE41 PRELIMINARY; PRT; 141 AA.

OBUE41;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
50S ribosomal protein L17.
RPLQ OR ATU1922 OR AGR.C_3516.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaces; Rhizobium.
NCBI_TaxID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002729; DUF48.

pfam; PF01867; DUF48; 1.

proDom; PF008695; DUF48; 1.

PTGRPAMs; TIGR00287; TIGR00287; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 343 AA; 38756 MW; 9DF5B16504974866 CRC64;
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   Agrobacterium
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Science 294:233-2328(2001).

EMBL; AE009146; AAL42918.1; -.
EMBL; AE008111; AAR87683.1; -.
INTERTO; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17; 1.
ProDom; PD004277; Ribosomal_L17; 1.
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Science
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                     white O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D. Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L. Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                             InterPro; IPR004441; rRNA_methyl_3.
InterPro; IPR001537; SpoU_methylase.
Pfam; PF00588; SpoU_methylase; 1.
Probom; PD001243; SpoU_methylase; 1.
                                                                                                                                                                                                                                            TIGR; DR0748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RWC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01167; RIBOSOMAL_L17; Ribosomal protein; Complete prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21608551;
                                                                                                                                                                                                                                                              Science 286:1571-1577(1999).
EMBL; AE001930; AAF10325.1;
                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus radiodurans Rl.";
                                                                                                             Transferase;
                                                                                                                                 TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA methyltransferase,
                                                                                                                                                                                                                                                                                                                                                       Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294:2317-2323(2001).
Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERLYTLGKRGDLHA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDRLYSIRTRGQIHS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
141 AA;
                                                                               TIGRO0186; rRNA_methyl_3; 1.
se; methyltransferase; Complete proteome.
246 AA; 26179 MW; 3E1827C743C6E3A8 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR00059; L17; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11743194;
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                      54.8%;
64.3%;
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family.
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Pred. No. 15;
6; Mismatches
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1;
Score 40; DB Pred. No. 27; 1; Mismatches
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27;
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4;
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    Indels
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Zalewski C.,
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QBLQX4

ID QBLQX
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AC QBLQX
DT 01-OC
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Best Local Similarity
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Q8GURO
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Query Match
                                                                                                    Submitted (MAR-2001) to the EMBL/GenBanl EMBL; AP003408; BAB93360.1; -. Gramene; QBLQK4; -. InterPro; IPR006047; Alpha_amyl_cat. InterPro; IPR006589; Alp_amyl_cat. InterPro; IPR006046; Glyco_hydro_13. Pfan; PF00128; Alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                                                               SMART;
                                                                                                                                                                                                                                                                 "Oryza sativa nipponbare(GA3) genomic
clone:B1131B07.";
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group). 
Bukaryota; Viridiplantae; Streptophyta; El 
Spermatophyta; Magnoliophyta; Liliopsida; 
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative alpha-amylase.
B1131B07.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Hydrolase; Glycosidase.
SIGNAL 1 15 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY171068; AA011776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Nanicao; TISSUE=Leaf; Vieira A. Jr., Nascimento J.R.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Musa acuminata (Banana)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-amylase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                                                         STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                              STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                Ehrhartoideae; Oryzeae; NCBI_TaxID=39947;
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01-MAR-2003
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                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8LQK4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4641;
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                                             SEQUENCE
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                                                                 SM00642;
                                                                                    PR00110; ALPHAAMYLASE
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416 AA;
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46558 MW;
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    54.8%;
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                                                                                                                                                                                                                                                                                                         Yamamoto
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/ta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up Last annotation 3.2.1.1).
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Pred. No.
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7D5ECE630F221915
    Score 40;
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                                               AEFD187910DD55C5 CRC64;
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47;
    DB
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i; Zingiberales; Musaceae;
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RESULT 18
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AC Q94AT
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OC SPETM
OC SPETM
OC SPETM
OC SPETM
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldrelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carnincia P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carnincia P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Blake J., Marinchan J., Mazzarelli J., Mombaerts P.,
RA Bushi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K., H., Weitz C., Whittaker C., Wilming L.,
RA Haysahizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Haysahizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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1700003E16Rik
1700003E16RIK.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative short-chain type dehydrogenase/reductase (
AT3G04000.
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"Functional annotation of a full-length mouse cDNA
"ature 409:685-690(2001).
EMBL; AK005628; BAP24157.1;
MGD; MGI:1919087; 1700003E16Rik.
SEQUENCE 506 AA; 55505 MW; 1AAA360DBCEDA709 CRC
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Mammalia; Eutheria;
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8; Conserv
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8; Conservative
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PubMed=11217851;
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Rodentia;
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5; Mismatches
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REQUENCE FROM N.A.

RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M., A Yamada K., Chan M.M., Chang C.C., Toriumi M., Wong C., Wu H.C., A Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M., Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W., A Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W., A Ecker J.R., Theologis A.;

Ra Ficker J.R., Theologis A.;

Ra Ecker J.R., Theologis A.;

Ra Ecker J.R., Theologis C. Tripp M.G., Wu T., Davis R.W., A Ecker J.R., Theologis Open Reading Frame (ORF) Clones.";

Ra Ecker J.R., Theologis A.;

Ra C. J.R., Theologis A.;

Ra C. J.R., Theologis C. Tripp M.G., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Davis R.W., A Light M.C., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., Wu T., W
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QSSCR2;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative short-chain type dehydrogenase/reductase.
T11118 11 OR AT3GO4000.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maggollophyta; Budloctyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
MCBI_TaxID-3702;
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L Carninci P., Chen H., Cheuk R., Hayasizaki Y., Ishida J., Jones Y., Kaminci P., Chen H., Cheuk R., Hayasizaki Y., Lin J., Kaminya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C., J., Sakurai T., Satou J., Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Ecker Seki M., Shinnozaki K., Davis R.W., Shinnozaki K., Davis R.W., Shinnozaki K., Davis R.W., Shi
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASE
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AY045807; AAK76481.2; -.

AY045807; AAK76481.2; -.

AYDFO016; ADH_Short.

TPF00106; ADH_Short; 1.

AYDFO0080; SDRFAMILY.
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                                                                                                                                                                          AA;
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Pred.
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Pred. No.
                                                                                                                                                                          1F0542EE7C599276 CRC64;
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      39;
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                                                          272;
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, Bowser L.,
Tones T.,
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Q9C425;
                                                                                                             Receptor.
SEQUENCE
                                                                                                                                                                  TISSUE=Brain;
strausberg R.;
                                                                                                                                                                                                                                                                                  Similar to nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A second reductase gene involved in melanin biosynthes sapstaining fungus, Ophiostoma floccosum."; Submitted (OCT-2000) to the EMBLYGENBAK/DDBJ databases -i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang H., Breuil C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezi
Ophiostomatales; Ophiostomataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reductase.
Ophiostoma floccosum.
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF317668; AAK07185.1; HSSP; Q12634; 1YBV.
                                                                                                                                         EMBL;
                                                                                                                                                       Strausberg
Submitted
                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00106; adh_short; 1 PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=104300;
                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO
Pfam; PF00106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                              134
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 365
                                                                                                                                       tted (DEC-2002) to the EMBL/GenBank/DDBJ databases BC041172; AAH41172.1; -
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                                                     7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            DRVFSVNTRGQ 144
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                                                                                                              45691 MW;
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                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F35E0E0E6004DCE2 CRC64;
                                                                                                              78EAE53CFB2358E7
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C -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR F

REMBL; AF492498; AAM90897.1; -.

R InterPro; IPR001536; Hormone_rec_lig.

R InterPro; IPR001723; Stdhrmn_receptor.

R InterPro; IPR001628; 2nf_C4steroid.

R Pfam; PF00104; hormone_rec; 1.

R Pfam; PF00105; zf-C4; 1.

R Pfam; PF00105; zf-C4; 1.

R PRINTS; PR00047; STROHORMONER.

R PRINTS; PR00047; STROHORMONER.

R PRINTS; PR00047; STROHORMONER.

R PRINTS; PR00035; Znf_C4steroid; 1.

R PRODOM; PD000035; Znf_C4; 1.

R PRODOM; PD000035; Znf_C4; 1.

R PROSITE; SM0039; Znf_C4; 1.

R PROSITE; SM0039; Znf_C4; 1.

R PROSITE; PS00031; NUCLEAR RECEPTOR; 1.

R PROSITE; PS00031; NUCLEAR PRODOM; PS00001; Tr

Transcription regulation; Zinc; Zinc-finger.

SEQUENCE 409 AA; 47056 MW; 156C9FAB92A46587 CRC64;
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-!- SIMILARITY: I
EMBL; AF492498; /
                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to protein kinases GCN2.
ISR1 OR P8283.9 OR YER106W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S Delius H., Dipaolo T., Dubois E., Dusterhoft A., Duncan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cholesterol and Bile Acids Regulate Xenosensor Signaling in D: mediated Induction of Cytochromes P450.";
J. Biol. Chem. 277:29561-29567(2002).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY
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MEDLINE-22162479; PubMed-12045201;
Handschin C., Podvinec M., Amherd
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                         STRAIN=S288C;
MEDLINE=97313271;
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Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                           SEQUENCE FROM N.A.
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53.8%;
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; Galliformes; Phasianidae; Phasianinae;
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Botstein
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OF CHARR-2003 (TrEMBLrel. 23, Last DE Nuclear receptor subfamily 1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Rodentia; f
                    RESULT
Q8BP65
ID Q8BP65
AC Q8
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Best Local S
Matches 8
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PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOW; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/thronics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jia Y., Cherry J.M.; to the Submitted (SEP-1997) to the -i- SIMILARITY: BELONGS TO TEMBL; U32445; AAB68076.1; -SGD; S0006310; ISR1.
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STRAIN=S288C;
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Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C;
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Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 57.
8; Conservative
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443 AA; 49735 MW;
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                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                          53.4%;
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Last annotation
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RESULT
Q9KY34
ID Q9
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STRAIN-C57BL/6J; TISSUE-Body;
X MEDLINE-23354683; PubMed=12466851;
X MEDLINE-23354683; PubMed=12466851;
A The FANTOM Consortium,
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Matches 7
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-1- SIMILARITY: BELONGS TO THE NUCLEAR HE
EMBL; BC012646; An4112646.1; -
MGD; MGI:1352462; Nr1h3.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR000935; Hormone_rec_lig.
InterPro; IPR001638; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00104; hormone_rec; 1.
Pfam; PF001105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR000047; STROIDFINGER.
PRODOM; PD000033; Znf_C4steroid; 1
SWART; SM00430; HOLL; 1.
SWART; SM00399; Znf_C4; 1.
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Q91X41;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
  Q9KY34
Q9KY34;
                                                                                                                                                                                                                                                                                        PROSITE; PS00196; COPPER_BLUE; 1.
PROSITE; PS00031. NUCLEAR_RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 445 AA; 50417 MW; 1A426DF38D935731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (AUG-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Matches 8
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J. Bacteriol. 183:5/2012.1; -.
EMBL; AF261825; AAK02042.1; -.
EMBL; AF261825; PR000209; Peptidase_S8.
InterPro; IPR000209; Peptidase_S8.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00136; SUBTILASE_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Eraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Putative membrane protei
                                                                                                                                                                                                                                               Boyd D., Peters G.A., Cloeckaert A., Boumedine K.S., Chaslus-Dancla E., Imberechts H., Mulvey M.R.; "Complete Nucleotide Sequence of a 43-Kilobase Genomic Island Associated with the Multidrug Resistance Region of Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ADT8;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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EMBL; AL939112; CAB92832.1; -.
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MEDLINE=21996410; PubMed=12000953;
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J. Bacteriol. 183:5725-5732(2001).
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Bacteria; Proteobacteria;
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                         "The gene duplication leading to present-day liver and muscle type genes of fructose-1,6-bisphosphatase occurred prior to the divergen of mammalia and amphibia."; submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ276513; CAB99413.1; -. HSSP; P00636; IPRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
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Pfam; PF01196; Ribosomal_L17; 1.
ProDom; PB004277; Ribosomal_L17; 1.
TIGRFAMS; TIGR00059; L17; 1.
PROSITE; PS01167; RIBOSOMAL_L17; 1.
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NCBI_TaxID=155892;
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STRAIN-ATCC 19089
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Best Local S
Matches 7
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STRAIN-NCC 2705;

MEDLINE-2224977; PubMed-12381787;

MEDLINE-2224977; PubMed-12381787;

MEDLINE-22224977; PubMed-12381787;

MEDLINE-22224977; PubMed-12381787;

Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,

Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

Pridmore R.D., Arigoni F.;

The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL; AEDI4794; ANN25396.1;

RIDOSOMBAI protein; Complete proteome.

RIDOSOMBAI POSTAIN COMPLETE PROTEOME.

RECOURAGE 177 AA; 19121 MW; 52F98D/C8F881F59 CRC64;
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ProDom; PD001491; In_FB_phphtase; 1.
Hydrolase.
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01-MAR-2003 (TREMBLrel. 23, Last sequence update)
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
50s ribosomal protein L17.
8PIQ OR BLISO7.
Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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49 ERLITFAKRGDLHS 62
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2: SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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AAW891957
AAR865475
AAR650521
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Rice alpha-amylase O. sativa alpha-amylase Partial alpha-amylase Rice alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Partial alpha-amylase Propionibacterium Human proteil Novel human proteil Novel human proteil Novel human proteil Propionibacterium Propionibacterium Human Protein segue Propionibacterium Propioniba

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RESULT 1
AAY93372
cereal grain. Weather damage is caused by the action of hydrolytic enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate the breakdown of starch granules and protein in the endosperm of germinating grain. Individual growers can identify areas of sprouting prior to harvest, preventing contamination of sound wheat by weather damaged wheat. The damaged grain can be harvested separately from the sound grain and financial losses resulting from down grading the whole crop can be avoided. The two-site immunoassays can be applied at mill or silo (elevator) receival of grain or can be used on farms with minimal
                                                                                                         The present sequence represents an epitope from the wheat alpha-amylase Antibodies which recognise the epitope are used in a two-site immunoassay for qualitative or quantitative detection of alpha-amylase in a test sample. The assay is used for detecting weather damage in a
                                                                                                                                                                                 Two site immunoassay for the qualitative or quantitative detection alpha-amylase in a test sample, used to detect weather damage in a cereal grain, such as wheat, rye, triticale or barley -
                                                                                                                                                             Claim
                                                                                                                                                                               cereal grain, such as wheat, rye,
                                                                                                                                                                                                                                                              (QUAL-) QUALITY WHEAT CRC LTD
                                                                                                                                                                                                                                                                                 11-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                           WO200028319-A1
                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                cereal grain
                                                                                                                                                                                                                                                                                                                                                                                           Epitope; wheat; alpha-amylase; two-site immunoassay; weather damage;
                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of an epitope of the wheat alpha-amylase
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Aspergillus fumiga
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                                                                                                                                                                    The present sequence represents a wheat alpha-amylase. Antibodies which recognise epitopes from this protein are used in a two-site immunoassay for qualitative or quantitative detection of alpha-amylase in a test sample. The assay is used for detecting weather damage in a cereal grain. Weather damage is caused by the action of hydrolytic enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate the breakdown of starch granules and protein in the endosperm of germinating grain. Individual growers can identify areas of sprouting prior to harvest, preventing contamination of sound wheat by weather damaged wheat. The damaged grain can be harvested separately from the contamination of firm of the contamination of sound wheat by meather the damaged grain can be harvested separately from the
                                                                                                                                                                                                                                                                                                                               sound grain and financial losses resulting from down grading the whole crop can be avoided. The two-site immunoassays can be applied at mill or silo (elevator) receival of grain or can be used on farms with minimal
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                                                                                                Sequence
                                                                                                                       equipment requirements.
                                                                                                                                                                                                                                                                                                            Disclosure;
146
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                        1 CRDDRPYADG
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Pred. No. 0.00038;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes encoding proteins involved in a plant polysaccharide
biosynthetic pathway, useful for modulating or altering the
polysaccharide content, composition or structure of the plant
  Rice; alpha-Amy6-C; alpha-Any7-C; alpha-Amy8-C; alpha-Amy10-C;
                                             Rice alpha-Amy7-C protein SEQ ID NO:2.
                                                                                                                                      AAB12798;
                                                                                                                                                                            AAB12798 standard; Protein; 428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 77; 301pp; English.
                                                                                           23-NOV-2000
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                                                                                                                                                                                                                                                                                      142 CRDDTEYSDG 151
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                                                                                                                                                                                                                                                                                                                                                                       Similarity 70. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention.
                                                                                        (first entry)
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Pred. No. 7.5;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a gene expression system containing the promoter region of an alpha-amylase gene; also described is a method for preparing a transgenic rice plant comprising: (1) infecting Agrobacterium into an unmatured embryo of a rice plant; (2) simultaneously culturing the embryo with a suspended culture of a dioctyledon during the transforming step; (3) growing the transformed embryo to a callus in a selective medium containing a plant growth hormone; and (4) regenerating the callus to roots and sprouts in a regeneration medium. The method can be used for mass production of a desired gene product in a plant host cell. The present sequence represents the rice alpha-Amy7-C protein, which is used in an example from the present invention.
  04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A gene expression system containing alpha-amylase gene, useful for mass product in a plant host cell -
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04-NOV-1993;
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                                             11-SEP-2001
                                                                                        US6288302-B1
                                                                                                                                                                                                                                                                Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                       Rice alpha-amylase (alpha-Amy7-C gene product).
                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2002 (first entry)
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cereal; brewing
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93JP-0297607
     98US-0072917
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26..428
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                                                                                                                                 Mature_protein
                                                                                                                                                                       Signal_peptide
                                                                                                                                                                                                                                                                                                                            rice;
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Pred. No. 48;
0; Mismatches
                                                                                                                                                                                                                                                                                                                               transgenic plant; angiosperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-amylase; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the promotor region of production of a desired gene
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Calpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C
C (see AAI70537). Expression of alpha-Amy7-C in cultured suspension
C cells of rice was induced 6-fold at day 12 after sugar depletion,
C and continued to increase up to day 14. The invention relates to
C the use of an alpha-amylase gene promoter and signal sequence in
C transgenic plant seeds. In a claimed method, a transgenic monocot
C is obtained by: transforming a nimmature embryo of the plant via
C alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that
C is induced under sugar-depleted or sugar-free conditions, a signal
C peptide sequence, and an exogenous sequence encoding a gene product;
C regenerating the transformed plant; and growing the transgenic
C sugar-free conditions. The gene product may also be obtained by
C cultivating an angiosperm host cell. The transgenic monocot plants

very
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Best Local S
Matches 8
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01-AUG-1995;
08-OCT-1997;
22-NOV-1994;
  (NASC-) NAT
                                                 13-FEB-1992;
                                                                         21-AUG-2000
                                                                                                TW402638-A.
                                                                                                                         Unidentified
                                                                                                                                                Alpha-amylase;
                                                                                                                                                                        Alpha-amylase related protein #1.
                                                                                                                                                                                                 31-JUL-2001
                                                                                                                                                                                                                         AAB97245;
                                                                                                                                                                                                                                               AAB97245 standard;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Column 61-64; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing a transgenic monocot plant comprising control of an alpha amylase promoter and signal provides transgenic plants particularly cereals
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)B; AAI70537.
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                                                                                                                                                                                                                                                                                                                                                         8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         428 AA;
  SCI COUNCIL
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95US-0509962.
97US-0947201.
94US-0343380.
                                                                                                                                                promoter; expression vector; rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chan M;
                         97TW-0101436
                                                 97TW-0101436
                                                                                                                                                                                                                                                Protein; 428 AA
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80.0%;
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Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                               Length
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RESULT 7
AAR76520
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a gene expression system comprising the alpha-amylase gene promoter. DNA encoding the signal peptide of alpha-amylase and the promoter along with the glucuronidase reporter gene and hygromycin resistance gene are used in the construction of a GUS gene expression vector, which when transformed into rice suspension-cultured cells, can be used to investigate the expression of the vector under the control of the promoter. The gene expression system can be used to conduct gene regulation and protein expression and secretion using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene expression system comprising the promoter region of alpha-amylase gene, produces large quantities of alpha-amylase in culture medium of sugar starved rice - \,
                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characteristics of the alpha-amylase gene promoter and the DNA sequence encoding the signal peptide. The present sequence represents an alpha-amylase related protein used in the course of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH20283
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                               06-JUN-1995
                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                      Misc-difference
                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                            Misc-difference
                                                   JP07143895-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                                                                                                                                                                                                             expression
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218
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                                                                                                                                                                                                                                                                         promoter; vector; heterologous;
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                         AA.
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04-NOV-1993;

93JP-0297607

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Matches

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Query Match
Best Local
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26-FEB-1988
15-JUL-1988
17-FEB-1989
05-MAY-1989
08-JUN-1989
22-OCT-1990
16-JAN-1991
26-JUL-1991
  WPI; 199
N-PSDB;
                                                                 Dawson WO,
Turpen AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virus; recombination; plant virus; alpha trichosanthin; phenotype; alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus; rice necrosis virus tobamovirus; gene expression; chinese cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR76519-R76521 represent the amylase gene products alpha-amylase-6-C, alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter regions of these amylase genes are used in a new gene expression system. The system may be used for the expression of heterologous genes in plant cells and for the large scale production of the encoded products of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 27-30; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene expression system contg. alpha-amylase gene promoter in plants for expression of heterologous genes  \label{eq:contgauge} % \begin{array}{c} (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) & (x,y) 
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                               (BIOS-) BIOSOURCE GENETICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice alpha-amylase coding
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12-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR55130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             some amino acids in this sequence appear to have been wrongly ared, see feature table and the corresp. DNA file AAQ92806,
     1994-176269/21
DB; AAQ65574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995-236472/31.
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8; Conser
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                                                                 Donson J,
Turpen TH;
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(first entry)
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91US-0641617.
91US-0737899.
91US-0739143.
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88US-0219279.
89US-0310881.
89US-0347637.
89US-0363138.
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                                                                                     Garger SJ,
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Pred. No. 48;
0; Mismatches
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                                                                                     Granthan GL,
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                                                                                     Grill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                     (DAWS/) DAWSON W O.

(DONS/) DONSON JO.

(GARG/) GARGER S J.

(GRAN/) GRANTHAM G L

(GRILL) GRILLE L K.

(TURP/) TURPEN A H.
                                                                                                                             WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The rice alpha-amylase gene may be inscreted into a recombinant plant virus which can then be used to infect plants for the production of non-native products (in this case alpha-amylase). Other genes which may be inserted into the virus are those which control a phenotypic trait, such as male sterility, or sequences encoding anti-sense RNA which can be useful to prevent the expression of undesired phenotypic traits. The recombinant virus is derived from a plus sense, single stranded virus selected from tobamovirus, brome mosic virus, rice necrosis virus or a genin virus.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant products; commercial production; fermentation; biosynthesis; natural products; recombinant proteins; product expression; protein expression; expressed proteins
                      Example 4; Page 96; 30pp; English
                                                              Recombinant plant viral nucleic acids - e.g. antibody or IL-1 in a plant
                                                                                                                                                                                            Donson J, Grille LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9303161-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR32987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Columns 53-56; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant plant viral nucleic acid - capable of infection and stable expression of non-native nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR32987 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal
                                                                                                                             1993-076518/09
DB; AAQ37680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 CRDD-PYGDG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                             Dawson WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0739143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US06359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%;
                                                                                                                                                                                                                Grantham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.5; D
Pred. No. 49;
0; Mismatches
                                                                                                                                                                                                                GL,
                                                                                                                                                                                                                Turpen
                                                                                     used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                TH,
                                                                                     ξ
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                                                                                     express a
                                                                                                                                                                                                                Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 433;
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                                                                                     prod.,
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01-AUG

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
22-OCT-1990;
16-JAN-1991;
26-JUL-1991;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant virus; alpha-haemoglobin; human; chinese cucumber; alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin; subgenomic promoter; coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Updated
(Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is rice alpha amylase. The coding sequence was inserted into a recombinant plant viral nucleic acid which was then used to express a recombinant product (in this case rice alpha-amylase) in a plant. The plant viral sequence may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean mottle, rice necrosis, geniniviruses, tomato golden mosaic, Cassava latent and
                                                                                                                                                                                                                                                                             Dawson
Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5589367-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW11871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW11871 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              maize streak viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1989;
31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice alpha-amylase
                                                                                                                                                 Recombinant viral DNA contains non-native
                                                                                                                                                                                                               N-PSDB; AAT61377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1989;
                                                               Example 4; Column 49-52; 42pp; English.
                                                                                                                             heterologous
                                                                                                                                                                                                                                                                                                                                          (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
sequences given duced by the reco
                                                                                                                                                                                                                                       1997-076845/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conserv
                                                                                                                                                                                                                                                                               AM,
                                                                                                                                                                                                                                                                                                                                            BIOSOURCE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRDD-PYGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRDDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AA;
                                                                                                                                                                                                                                                                               Donson
Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first end
                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                  89US-0310881

89US-0347637

89US-0343138

92US-0923692

88US-0160766

88US-0160771

88US-0219279

90US-0600244

91US-0641617

91US-0737899

91US-0739143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0184237
                                                                                                                                                                                                                                                                                 J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
  in AAW11868-71 represent proteins which were ombinant viruses of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                             and
                                                                                                                             for altering plant phenotype or protein prodn
sub-genomic promoter for expression of
and native promoter for expression of coat
                                                                                                                                                                                                                                                                                                   Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.5; I
Pred. No. 49;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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t PI field.)
                                                                                                                                                                                                                                                                                                     Granthan
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                                                                                                                                                                                                                                                                                                     GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                     Grill LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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produced

recombinant viruses

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RESULT 11
AAY01375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses are recombinant plant viruses which comprise a native plant virus subgenomic promoter, at least one non-native plant virus subgenomic promoter, and a sequence encoding a plant virus coat protein. These heterologous sequences are preferably under the control of the native promoter sequence. By using a plant virus existing cells can be altered with a new coding sequences without involving germ cell. The recombinant viruses are stable and can cause systemic infection, with stable expression/transcription in plants that are hosts for the non-native part of the vector. The nucleotide sequences encoding these protein preferably integrated in plant viruses having either the O-coat protein or the UI-coat
                                                                                                                               19-JAN-1994;
26-FEB-1988;
26-FEB-1988;
15-JUL-1990;
16-JAN-1991;
26-JUL-1991;
01-AUG-1991;
      Recombinant plant viral nucleic acid derived from a plus sense, single stranded RNA plant virus - useful for the transcription products in a host
                                                                               Dawson
Turpen

 sativa alpha-amylase

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein gene.

"Thated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2003
04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01375;
                                                N-PSDB;
                                                                                                                                                                                                                08-JUN-1989;
31-JUL-1992;
                                                                                                                                                                                                                                                                                                           US5889190-A
                                                                                                                                                                                                                                                                                                                              Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY01375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                          WPI; 1999-243290/20
                                                                                                                                                                                                                                      05-MAY-1989
                                                                                                                                                                                                                                              17-FEB-1989;
                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                       30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                  transcription;
                                                                                                                                                                                                                                                                                                                                                              Recombinant;
                                                                                                             (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                               AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                 AAX29144
                                                                                                             BIOSOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRDD-PYGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRDDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                               Turpenth;
                                                                                           Donson
                                                                                                                                                                                                                                                                                                                                                           plant virus;
                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                               89US-0363138.
92US-0926592
94US-0184237.
88US-0160766.
88US-0160771.
88US-0219279.
90US-0600244.
91US-0737899.
91US-0739143.
                                                                                                                                                                                                                                                                                                                                                  therapeutic;
                                                                                                                                                                                                                                     89US-0310881
89US-0347637
                                                                                                                                                                                                                                                                    95US-0480432
                                                                                                              TECHNOLOGIES
                                                                                           J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to correct
                                                                                          Garger
                                                                                                                                                                                                                                                                                                                                                  coat protein; systemic infection;
c; rice; alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.5;
Pred. No. 49;
                                                                                           SJ,
                                                                                                               INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF field.)
PR field.)
                                                                                           Grantham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                           GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲:
                                                                                           Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                     of
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Example 4;

Columns 47-51; 46pp; English.

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                                                                            31-JUL-1992;
26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
17-FEB-1989;
05-MAY-1989;
08-JUN-1989;
22-OCT-1990;
16-JAN-1991;
             Dawson
Turpen
                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                Rice; alpha-amylase; systemic infection;
                                                                                                                                                                                                                                                                                 AAW84383 standard; Protein; 434
                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                     02-FEB-1999
                                                                                                                                                                                   US5866785-A
                                                                                                                                                                                                                                      Rice alpha-amylase sequence.
                                                                                                                                                                                                                                                      01-APR-1999
                                                                                                                                                                                                                                                                    AAW84383;
                                    (BIOS-)
                                                                                                                                                                                                                                                                                                                      155 CRDD-PYGDG
             AM,
                                    BIOSOURCE TECHNOLOGIES INC.
             Donson J,
Turpen TH;
                                                                                                                                                                                                                                                     (first entry)
                                                9205-0923692
88US-0160771
88US-0150771
88US-0119279
89US-0310881
89US-0347637
89US-0347637
89US-0647637
99US-0647637
91US-0739143
94US-0739143
94US-0739143
94US-0739143
                                                                                                                                                        95US-0482920
                                                                                                                                                                                                               plant virus; RNA plant virus promoter; foreign gene expression; AIDS therapeutic drug
                    Garger
                     SJ,
                     Granthan GL,
                     Grill LK
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RESULT 13
AAV87792
ID AAY87792
XX AAV87792
AC AAY87
AC AAY87
AC AAY87
AC Rice
XX Anine
KW Inten
KW Inten
KW Stert
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XX INTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
                                                                                                                                                17 FEB-1989
08-JUN-1989
26 FEB-1988
26 FEB-1988
15 -JUL-1988
05 -MAY-1988
05 -MAY-1989
22 -OCT-1990
16 -JANG-1991
01 -AUG-1991
31 -JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents rice alpha-amylase. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs.
                        Garger
Donson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6054566-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Animal RNA virus; viral coat protein; plant; male sterility; interleukin; EPO; erythropoletin; CSF; colony stimulating factor; Factor VIII, hGH; human growth hormone; melanin; insulin; vaccine; stereo specific catalysis; alpha-amylase; rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY87792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY87792 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant plant viral vector - that is capable of systemic infection in host plant and stable production of heterologous DNA useful for producing therapeutic proteins for treating e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX03386.
                                                                                                   (BIOS-) BIOSOURCE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 - AUG - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 CRDD-PYGDG
                        J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Columns 51-54; 45pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AA;
                                                   Grill LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                88US-0160766.
88US-0160771.
88US-0219279.
88US-0219279.
89US-0347637.
90US-0600244.
91US-0641617.
91US-0737899.
91US-0739143.
                                                                                                                                                                                                                                                                                                                                                                                      89US-0310881
89US-0363138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0484341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                Turpen TH, Granthan GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0%;
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Pred. No. 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                Dawson WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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1 CRDDRPYADG 10

Query Match Best Local S Matches 8

h 68.0%; Similarity 80.0%; 8; Conservative

Score 41.5; D Pred. No. 49; 0; Mismatches

DB 20; 1;

Length 434; Indels

1;

1;

Sequence unnecessary (Updated on

434 AA;

20-MAR-2003 to

correct PR field.)

CC from a plus sense, single stranded RNA plant viral nucleic acid derived crown a plus sense, single stranded RNA plant virus. The recombinant plant crown a plus sense, single stranded RNA plant virus and promoter comparison acid comprises: (a) a first plant viral subgenomic promoter coperably joined to a first nucleic acid expression sequence; and (b) a second plant viral subgenomic promoter that is non-native and is operably of the second nucleic acid expression sequence; where, (i) (a) and (c) are incapable of recombination with one another; (ii) either the first or the second nucleic acid expression sequence is a plant viral comparison of protein coding sequence. The recombinant plant viral nucleic acid cother useful polypeptides or proteins e.g. enzymes, complex biomolecules and ribozymes. It also gives the option of applying the coding sequence coding sequences and is capable of systemic infection in the plant host. The transformation and regeneration of target organisms become

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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel recombinant viral nucleic acid (I) CC from a non-retroviral (+) sense, single stranded animal RNA virus comprising a nucleic acid sequence coding for a viral coat protein CC comprising a nucleic acid sequence coding for a viral coat protein CC nucleic acid sequences regulated by two other subgenomic promoters. CC nucleic acid sequences regulated by two other subgenomic promoters. CC (I) is useful for expressing foreign genes e.g. genes inducing male CC interleukins, EPO (erythropoietin), CSF (colony stimulating factor), CC factor VIII, hGH (human growth hormone), melanin, insulin, vaccines CC etc., and enzymes that are useful for stereo specific catalysis of CC organic compounds. (I) is stable and transcribed systemically. The dual CC subgenomic promoter system reduces the frequency of recombination thus reducing regeneration of the wild type virus. This sequence represents a rice alpha-amylase protein which is described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                        (DASP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant non-retroviral nucleic acid for producing proteins such interleukins, melanin and vaccines, comprises subgenomic promoters linked to sequences coding for viral coat protein and heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linked to sequences
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             Claim 26;
                                                                             N-PSDB;
                                                                                        WPI;
                                                                                                               Gausing K,
                                                                                                                                                                             24-APR-1989;
                                                                                                                                                                                                     24-APR-1990;
                                                                                                                                                                                                                               01-NOV-1990
                                                                                                                                                                                                                                                       W09012876-A
                                                                                                                                                                                                                                                                                Solanum tuberosum
                                                                                                                                                                                                                                                                                                        potato; alpha-amylase;
                                                                                                                                                                                                                                                                                                                               Partial alpha-amylase precursor coded by clone
                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                             AAR07669;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR07669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                     used
                                    fragments encoding alpha-amylase in dicotyledonous plants used for detecting gene organisation {\tt etc.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-338510/29
DB; AAA12394.
                                                                          1990-348479/46
DB; AAQ06479.
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                                                                                                                                        DANSKE SPRITFABRIKKER DANISCO A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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             Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434
                                                                                                               Kreiberg
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(first entry)
             4;
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                                                                                                                                                                               89DK-0001980
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             lpp;
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                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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             English
                                                                                                                                                                                                                                                                                                       starch degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Pred. No. 49;
                                                                                                                                                      DANISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                 Amyz6 from potato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434;
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RESULT 15
ABB59190
ID ABB59
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amy26 was isolated from a cDNA library prepared from RNA extracted from sprouts of a potato. The library was screened with a barley alpha amylase probe. The nucleic acid sequence encodes a partial alpha-amylase procursor commencing at amino acid residue 133 of the full-length protein.

See also AAQ06476-8 and AAQ06553.
                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL/1876-ABL/3051), expressed DNA sequences (ABL/1840-ABL/1875) and the encoded proteins (ABB/187737-ABB/2072).
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB59190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB59190 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct
                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                             Disclosure; SEQ ID NO 4362; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
N-PSDB; ABL03293.
                                                                                                                                                                                                                                                                                             Venter
                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
Sequence
                                                                                                                                                                                                                 genes from Drosophila
                                                                                                                                                                                                                              New isolated nucleic acid
                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                             JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKDDTQYSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AA;
  594
                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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2000US-0614150
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                                                                                                                                                                                                                                                                                              , DWD
                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 core 41; DB red. No. 29; Mismatches
                                                                                                                                                                                                                                                                                             Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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29;
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                                                                                                                              invention alling and
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                                          WIPO
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Query Match Best Local S Matches 6

Similarity 6; Conserv

Conservative

63.9%; 66.7%;

Score 39; DB 22; Pred. No. 1.9e+02;

Length 594; Indels

0;

Gaps

0;

Mismatches

δ

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RESULT 16
AAM50253
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                                                            The present sequence is that of alpha-amylase encoded by DNA clone alpha-Amy3-C (See AAT/0540). Expression of alpha-Amy3-C increases 5-fold following sugar starvation. The invention relates to the production of recombinant proteins in transgenic plants and transgenic plant seeds. In a claimed method, a transgenic plants and transgenic plant seeds. In a claimed method, a transgenic monocot is a dyrobacterium-mediated transformation with DNA comprising a plant aprobacterium-mediated transformation with DNA comprising a plant is induced under sugar-depleted or sugar-free conditions, a signal peptide sequence, and an exogenous sequence encoding a gene product; regenerating the transformed plant; and growing the transgenic plant, which expresses the gene product may also be obtained by cultivating an anglosperm host cell. The transgenic monocot plants are especially useful in brewing and to produce glucose from starch.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1992;
01-AUG-1995;
08-OCT-1997;
22-NOV-1994;
                                                                                                                                                                                                                                                                                                                             Producing a transgenic monocot plant comprising a transgene under control of an alpha amylase promoter and signal peptide sequences, provides transgenic plants particularly cereals for the brewing industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM50253 standard; Protein; 435
                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
monocot; cereal; brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50253;
                                                                                                                                                                                                                                                                                               Disclosure; Column 79-82; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NASC-) NAT SCI COUNCIL ROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice alpha-amylase (alpha-Amy3-C gene product).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                             2001-647191/74.
DB; AAI70540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu L, Chan M;
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95US-0509962.
97US-0947201.
94US-0343380.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
26..428
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 62
60
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Score
Pred.
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38;
DB 22;
2e+02;
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RESULT 17
AAB97247
ID 97247
XX AAB97
AX AAB97
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RESULT 18
AAW81063
ID AAW81
XX
AC AAW81
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DT 02-JU
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a gene expression system comprising the alpha-amylase gene promoter. DNA encoding the signal peptide of alpha-amylase and the promoter along with the glucuronidase reporter gene and hygromycin resistance gene are used in the construction of a GUS gene expression vector, which when transformed into rice suspension-cultured cells, can be used to investigate the expression of the vector under the control of the promoter. The gene expression of the vector under the conduct gene regulation and protein expression and secretion using the characteristics of the alpha-amylase gene promoter and the DNA sequence encoding the signal peptide. The present sequence represents an alpha-amylase related protein used in the course of the present reports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu S,
   02-JUN-1999
                                                        AAW81063;
                                                                                                       AAW81063
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12; 104pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene expression system comprising the promoter region of alpha-amylase gene, produces large quantities of alpha-amylase in culture medium of sugar starved rice .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-167365/17.
N-PSDB; AAH20285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NASC-) NAT SCI COUNCIL.
                                                                                                                                                                                                                                          148 CSDDTQYSDG
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                                                                                                                                                                                                                                                                                            1 CRDDRPYADG 10
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                                                                                                                                                                                                                                                                                                                                              Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 AA;
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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(first entry)
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                                                                                                          Protein; 1036 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                       62.3%;
                                                                                                                                                                                                                                                                                                                                              Score 38; DB 22;
Pred. No. 2e+02;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                Length 435;
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CC polypeptide (SP) used in the method of the invention. The SPs can CC polypeptide (SP) used in the method of the invention or survival CC of a cell which expresses the SP. The products can be used to CC modulate spermatogenesis, osteogenesis, chondrogenesis or neuronal cells, e.g. CC modulate spermatogenesis. They can be used for treating e.g. CC cell differentiation or to enhance survival of neuronal cells, e.g. CC degenerative disorders marked by loss of particular cell-types, CC degenerative disorders marked by loss of particular cell-types, CC they can be used to treat neurological conditions derived from CC acute, subacute, or chronic injury to the nervous system, aging of CC acute, subacute, or chronic injury to the nervous system, aging of CC the nervous system chronic inmunological diseases of the nervous system or affecting the nervous system. They can also treat be used to CNS trauma infarction, infection (such as viral infection with CC varicella-zoster), metabolic disease, nutritional deficiency, cor in nerve prostheses for the repair of central and peripheral CC or in nerve prostheses for the repair and regeneration of lung the nervous, pendymonas and for liver repair and regeneration of lung constants.
RESULT 19
ABB59323
ID ABB59
XX
AC ABB59
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell proliferation; cell differentiation; spermatogenesis;
osteogenesis; chondrogenesis; apoptosis; degenerative disorder;
neoplastic disorder; hyperplastic disorder; varicella-zoster;
  ABB59323;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                          formation, .... for detection,
                                                                                                                                                                                                                             tumours, ependymonas and for liver repair which the treatment of emphysema, or for enhancing formation, tissue formation or fertility. The products diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated smoothened genes - used to develop products for treating e.g. cancers, neurodegenerative disorders, nervous system injury, immunological diseases or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1997;
01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour; liver repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; smoothened
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino
                             ABB59323 standard; Protein; 1036 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (VHEU/)
                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-105996/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is the amino acid sequence of the novel Drosophila smoothened septide (SP) used in the method of the invention. The SPs can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                 89
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ONTOGENY INC.
VAN DEN HEUVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV99968
                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages 94-97; 107pp; English.
                                                                                               RDDKPWFDG
                                                                                                                         RDDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of
                                                                                                                                                                                                            1036 AA;
                                                                                                                                                     Conservative
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97US-0051407.
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                                                                                                                                                                 62.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Drosophila smoothened
                                                                                                                                                    Score 38; DB Pred. No. 4.9e 2; Mismatches
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                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                 DB
                                                                                                                                                                                 20;
                                                                                                                                                                               Length 1036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                  bond
can also be
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                                                                                                                                                     Gaps
                                                                                                                                                     0;
                                                                                                                                                                                                                       RESULT 20
AAB28647
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57037-ABB72072).

(ABB57037-ABB72072).
                                                                                    cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 4761.
    24-OCT-2000
                             US6136958-A
                                                                                                                          Drosophila
                                                                                                                                                       13-FEB-2001
                                                                                                                                                                                  AAB28647;
                                                                                                                                                                                                            AAB28647 standard; Protein; 1036
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  specification, but was obtained in electronic
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL03426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                       Drosophila melanogaster
                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000;
                                                                                  signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-656860/75
                                                                                                                                                                                                                                                                               68 RDDKPWFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JC,
                                                                                                                                                                                                                                                                                                       2 RDDRPYADG
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                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                          Smoothened.
                                                                                                                                                                                                                                                                                                                                                                                        1036 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4761; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
                                                                                                 Smoothened;
                                                                                                                                                                                                                                                                                                                                     Conservative
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2000US-0614150
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                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                               76
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                                                                                                                                                                                                                                                                                                                                               62.3%;
66.7%;
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                                                                                                 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                               proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                Score 38; DB 22;
Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                             AA
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                                                                                                                                                                                                                                                                                                                                                            Length 1036;
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invention

and 1S cell-cell

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Best Local S
Matches 6
Peptides are Abs raised to them are useful in detecting the presence of NGF and precursors, allowing early diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                              21
159
                                       Disclosure;
                                                                    New peptide fragments of nerve growth factor or its precursor used to raise specific antibodies for immunoassay, esp. for brain
                                                                                                                              Olson L,
                                                                                                                                                                                                                                                                                                                                                                                    AAR07159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence was used for comparison studies with vertebrate Smoothened polypeptides. Smoothened interacts with Hedgehog and Patched signalling molecules involved in cell proliferation and differentiation. Brat Smoothened cDNA was isolated from an embryonic day 9-10 rat cDNA library. The rat smoothened cDNA was then used as a probe to isolate the human homologue from a human embryonic lung cDNA library. Antibodies which specifically bind to the vertebrate smoothened polypeptides were identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies to vertebrae smoothened proteins and patched signaling molecules involved in differentiation -
                                                                                                          WPI; 1990-304983/40
                                                                                                                                                      (LOPE-) LOPE MED AB
                                                                                                                                                                             14-MAR-1989;
                                                                                                                                                                                                   08-MAR-1990;
                                                                                                                                                                                                                        20-SEP-1990
                                                                                                                                                                                                                                               WO9010644-A.
                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                          Nervous disorders; Alzheimer's disease; Parkinson's disease; stroke
                                                                                                                                                                                                                                                                                                                Synthetic Nerve growth factor (NGF) peptide fragment.
                                                                                                                                                                                                                                                                                                                                        24-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                AAR07159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 5; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                              RDDKPWFDG
                                                                                                                             Persson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Sauvage FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1036 AA;
                                    Page 11; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                             89SE-0000899
                                                                                                                                                                                                   90WO-0000149
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                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                                                                                                                                                                                                                                                                                   protein; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.3%;
                                                                                                                               Ebendal T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB
Pred. No. 4.9e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenthal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; L
4.9e+02;
thes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which relate to Hedgehog cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1036;
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RESULT 22
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                                                                              Query Match
Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1991;
12-JUL-1991;
23-JUL-1991;
28-AUG-1991;
20-SEP-1991;
14-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous disorders eg. Alzheimer's and Parkinson's disease, cord injury, stroke etc.
Peptide corresponds to AAs 54 to 69 of chicken NGF.
                                                                                                                                                                                                                               Oligonucleotide probes and primers were synthesised based on the NT family including NGF, BDNF and NT-3. These were used to isolate DNA encoding NT-4 from nucleic acid from Xenopus ovaries. This DNA was then used to isolate other mammalian DNA encoding NT-4, including human NT-4 DNA.
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 96-97; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Use of neurotrophin-4 for promoting growth and survival of cells - useful in treating neurological, fertility and immunological disorders and in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hallbook F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurotrophin;
brain-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
22-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGF, chicken.
                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1992-415468/50.
DB; AAQ32200.
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                                                                                                                                                                 42 AA;
                                                                                Conservative
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91US-0734422.
91US-0751356.
91US-0762674.
91US-0791924.
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Pred. No.
1; Mismatc
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                                                                              Score 37; DB Pred. No. 26; 1; Mismatches
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cor; BDNF;
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                     Chicken mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP71159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds. This peptide was designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-320328/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1992;
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22-APR-1994
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                                                                                                                                                                                                          Proneurotrophin; nerve growth factor; NGF; neurotrophin; NT-3; NT4; NT5 brain derived neurotrophic factor; BDNF; vasotropic; cerebroprotective; antimicrobial; cardiant; virucide; antibacterial; neuroprotective; MMP; nootropic; antiinflammatory; anticonvulsant; plasminogen; plasmin; p75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP71159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SOLO/) SOLOMON
                                     W0200296356-A2
                                                                                                        Gallus sp.
                                                                                                                                                                            apoptosis;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                chicken.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 118
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50.0%;
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ABR41533
ID ABR41
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Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder;

Human DITHP protein modification/maintenance protein.

02-JUN-2003 ABR41533;

(first entry)

ABR41533 standard; Protein; 346

57

CRDPRPVSSG

1 CRDDRPYADG

10 66

0;

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CC of a proneurotrophin, where PD comprises a pro-domain conserved region, CC or a modified proneurotrophin protein (ID) with a PD, a mature CC onserved region to MD and resistant to protease cleavage. The PD is CC selected from specific peptide fragments of human nerve growth factor (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin 4/5 (NT4/5). (ID) is useful for inducing CC apoptosis in a cell comprising P75 receptors (normal number or higher CC than the normal number of p75 receptors) on its surface, by causing the P75 receptor to bind (ID), in vitro, in mammals or humans. The method is CC useful for tracating vascular smooth muscle plaque e.g. atherosclerotic CC plaque. The cell is a malignant cell e.g. cells of tumour, melanoma, CC prostate, pancreas, nervous system (e.g. medulloblastoma or astrocytoma), CC leukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte, heart, vascular smooth muscle or neural cell. A molecule that inhibits CC the binding of proneurotrophin to a p75 receptor is useful in a method CC or inhibiting apoptosis of a cell in a mammal e.g. human suffering from CC condition associated with undesired apoptosis due to binding of a proneurotrophin to p75 receptor. The condition is the result of an injury counsed by a chemical or radiation or occurring during cancer treatment. Howaiic
Matches
                  Query Match
Best Local
                                                                                                                        chemical or radiation or occurring during cancer treatment, hypoxic ischaemia caused by stroke or heart attack, viral or microbial infection, meningitis, encephalitis or abscesses, neurodegenerative disorders e.g. Alzheimer's disease, familial dysautonomia, ataxia telangiectasia, Charcot-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular atrophy or Friedriech's ataxia, or multiple sclerosis, convulsions, epilepsy and spinal cord injury. Sequences ABP71151-60 represent pro and mature domains of NGF from various species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein for inducing apoptosis, has proneurotrophin pro-domain with conserved regions, mature neurotrophin domain, and connector the joins conserved region to mature domain and resistant to protease
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13-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
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                                                                                   Sequence
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Similarity 6; Conserv
                                                                                      118 AA;
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  Conservative
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2001US-305510P
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                    .0%;
Score 37; DB Pred. No. 77; 1; Mismatches
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                                           24;
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CC The invention relates to novel human diagnostic and therapeutic CC polynucleotides designated dithp (ACC46049) and to their CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates CC to polynucleotide sequences at least 90% identical to the dithp cDNA CC sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising dithp nucleic acid sequences; methods of transgenic organisms comprising dithp nucleic acid sequence; methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein may be used in the CC assessing the toxicity of test compounds using a dithp hybridisation CC diagnosis of a wide variety of conditions including cancer and other cell proble. Dithp nucleic acid sequences and DITHP proteins may be used in the CC vital, fungal or parasitic infections; hormonal disorders; methodic CC disorders; autoimmune or inflammatory disorders; metabolic CC disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP coteins can additionally be used in analysis of the proteome of a tissue CC or cell type and to induce antibodies. The dithp nucleic acids are cell type and to induce antibodies. The dithp nucleic acids are protein scan additionally be used in analysis of the proteome of a tissue of protein scan in madels of human disease or knock in CC protein modification and/or maintenance.

CC The present sequence represents a DITHP protein modification and/or maintenance.

CC The present sequence represents a DITHP protein modification for this patent did not form part of the printed constraint protein modification and/or maintenance.
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19-JUN-2001;
20-JUN-2001;
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29-MAR-2001;
29-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies
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Peralta CH,
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17-MAY-2001;
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DB; ACC46471.
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Hillman
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LO A,
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TP, Nguyen DA, Kre.
TP, Nguyen DA, Panzer
TN, Chen AJ, Panzer
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O, Yap PE, Amsl
DA, Kleefeld Y,
AJ, Panzer SR,
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sorder; transport disorder;
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Matches 5
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14-MAR-2001;
10-AUG-2001;
19-SEP-2001;
26-SEP-2001;
26-SEP-2001;
26-SEP-2001;
The present invention relates to a new|method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer (e.g. patients having a familial history of varian cancer markers may be used in the management and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; halbeimer's disease; parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; stakenic heart disorder; thereosclerysis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                                                                                                                 Assessing whether a patient is afflicted with ovarian cancer, useful ir assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient -
                                                                                                                                                                                                                                                                                                                                        Disclosure;
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)B; ABS76439.
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                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gannavarapu M, Hoersch S, Kamatkar S, K
Morrisey MP, Olandt PJ, Sen A, Vieby PO,
u K, Schmandt RE, Zhao X, Glatt K;
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2001US-276026P.
2001US-311732P.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoskeleton associated protein; CYSKP-12; cancer; proliferative; autoimmunity; inflammatory, vesicle trafficking; neurological; cardiovascular; cell motility; reproductive; muscle disorder.
                                                                                                                                                     Binding-site
                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2000
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                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDYRPYAD 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 AA;
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188
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87.5%;
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Pred. No.
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phosphorylation site'
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                                                   phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylation site"
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2.8e+02;
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RESULT 28
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standard;

Protein;

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25-MAR-2003 AAR48673; AAR48673

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                                                     Matches
                                                                                                                                                                                                                                          AAY91946-61 show human cytoskeleton associated proteins 1 to 16 (CYSKP-1 to CYSKP-16) respectively. The sequences can be used to treat and diagnose cancer and cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cardiovascular, cell motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-2 to CYSKP-16 can be used to treat or prevent disorders associated with
                                                                                                                                                                                                                                                                                                                                                                 Human cytoskeleton associated proteins, used to treat cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive and muscle disorders
                                                                                                                                              diabetes mellitus, Goodpasture's syndrome, osteoarthritis, and trauma. CYSKP antagonists can be used to treat or prevdisorder associated with increased expression or activity c
                                                                                                                                                                                      trafficking, neurological, cardiovascular, cell motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-2 to CYSKP-16 can be used to treat or prevent disorders associated with decreased expression or activity of CYSKP (claimed), for example, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, cancers, autoimmune/antiinflammatory disorders such as allergies, anemia, asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease,
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 94-95; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA08592.
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Guegler KJ, Patterson
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27-APR-1999;
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99US-0131321
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Azimzai Y,
                                                    Score 37; DB Pred. No. 3.1e 0; Mismatches
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                                                                     3.1e+02;
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Baughn MR;
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vesicle trafficking,
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lty of CYSKP
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The granulin inhibits keratinocytes and is useful for promoting the healing of wounds (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granulin; keratinocytes; wound healing; inhibition; peptide; granulocytes; leucocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Granulin sequence
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                          Human GP88 autocrine growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 4c; 53pp; English.
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N-PSDB; AAQ49052.
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                       WO9852607-A1
                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                  AAW85475 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SOLO/) SOLOMON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-1992;
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                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                      15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 CRDNRGGWACCPYAQG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRDDR-----PYADG 10
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                                              /note= "E19V peptide used to 566..579 /note= "A14R peptide used to
                                                                                                                 Location/Qualifiers 340..364
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50.0%;
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Pred. No.
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                                                                                            used to raise antibody"
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4.1e+02;
                                                         raise antibody"
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  28-FEB-2002
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RESULT 30
AAE20521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition containing antagonist of growth factor GP88 - useful for
treating cancer and viral diseases and also for diagnosing disease
from altered GP88 expression
                                                               Region
                                                                                                                                                                           Human; granulin
antineoplastic;
                                                                                                                                                                                                                             Human granulin/epithelin precursor (GP88) protein.
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23-MAY-1997;
US2002025543-A1
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                01-JUL-2002
                                                                                                                                                                                                                                                                                                                              AAE20521 standard; Protein; 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               altered GP88 activity.
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DB; AAV82825.
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97US-0863079
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                                                                                              Location/Qualifiers 273
                                                                                                                                                                             precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antioestrogen therapy; skin cancer.
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                                                           /note= "Encoded by AAG" | 346.364
                              /note= "Region used as antigen
GP88 neutralising antibody"
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50.0%;
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4.1e+02;
                                                to develop anti-human
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Matches 8
                                                                                                                                                                                                                                                                     The invention relates to a method for diagnosing tumourigenicity in a human. The method comprises obtaining a biological sample containing cells from the patient, detecting GPB8 in the cells of the sample, and determining the number of GPB8 positive cells in the sample, and determining the ratio of GPB8 positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of anticestrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPB8, or less than 5 % GPB8 positive cells. The present sequence is human granulin/epithelin precursor (GPB8) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing tumorigenicity in a human, comprising obtaining a cell sample, detecting GP88 in the cells, and determining the number of GP88 positive cells in the sample - \,
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N-PSDB; AAD32850.
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08-DEC-1999;
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                                                                                                                                                 Local Similarity 50.0 nes 8; Conservative
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99US-0456886.
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Pred. No. 4.1e+02;
1; Mismatches 1;
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Result No.

RESULT 1 US-07-973-324A-4

ALIGNMENTS

Sequence 4, Application US/07973324A Patent No. 5460952 GENERAL INFORMATION:

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

STREET:

Chicago

Illinois

ADDRESSEE:

E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive

COUNTRY: STATE:

RY: United States of America 60606-6402

```
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
                                                                                                                                     TITLE OF INVENTION: Gene Expression System Comprising the TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BORUN, MICHAEL F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 3114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                   CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/639,792
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,
                                                          APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 428 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/4
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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22-NOV-1994
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  38,153
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Pred. No. 9.
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1 CRDDRPYADG 10

149

CRDD-PYGDG 157

Matches Query Match

Best Local Similarity
Matches 8; Conserv

Conservative

0;

Mismatches

Indels

68.0%;

Score 41.5; D Pred. No. 9.8;

US-08-343-380-4

Sequence 4, Application US/08343380 Patent No. 5712112

GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei

CORRESPONDENCE ADDRESS:

STREET:

Chicago

ADDRESSEE:

E: Marshall, O'Toc 6300 Sears Tower,

O'Toole, lower, 233

Gerstein, Murray & Borun South Wacker Drive

STATE: COUNTRY:

Illinois

60606-6402

States of America

US-07-973-324A-4

TYPE: amino a TOPOLOGY: lir MOLECULE TYPE:

amino acid

linear

protein

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ_ID_NO: 4:

SEQUENCE CHARACTERISTICS

LENGTH:

428 amino acids

REFERENCE/DOCKET NUMBER: 31: TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448

NAME: Borun, Michael F. REGISTRATION NUMBER: 25447

31149

APPLICATION NUMBER: US/0; FILING DATE: 04-NOV-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:

SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:

OPERATING SYSTEM: COMPUTER:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

Release #1.0, Version #1.25

US/07/973,324A

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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APPLICANT: Yu, Surma,
APPLICANT: Liu, Li-Fei
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Chan, Ming-Tsair
APPLICANT: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Plant Seeds
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STEET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                TELEFAX: (312) 47-04-04-08

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
HOLECULE TYPE: protein
US-09-072-917A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-072-435-4
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: (312) 474-6300
TELLEPAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
Query Match 68.0%; Score 41.5; D
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09072917A Patent No. 6288302 GENERAL INFORMATION:
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Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PAPPLICATION UNBER: US 08/509,962
PRILING DATE: 01-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/3425
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    TELEPHONE:
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149 CRDD-PYGDG 157
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Pred. No. 9.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      28123/34257
                                              DB 3; Length 428;
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1; Indels
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Gaps
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RESULT 5
US-07-923-692C-6
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; MOLECULE TYPE: protein US-07-923-692C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
GENERAL I
                                                                                                                                            TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
BAPLICATION DATA:
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donson, Jon
APPLICANT: Dawson, William 0.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-JUL-1988 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION NIMBER: US 160,766
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                                                               TYPE: amı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Halluin, Albert REGISTRATION NUMBER: :
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FILING DATE: 08-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 347,637 FILING DATE: 05-MAY-1989
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ZIP: 94111
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149 CRDD-PYGDG 157
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                                                                                                        : 434 amino acids
amino acid
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26-FEB-1988
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FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600
FILING DATE: 22-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 641
FILING DATE: 16-JAN-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                              APPLICATION NUMBER: US 2: FILING DATE: 15-JUL-1988 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 1
FILING DATE: 26-FEB-1988
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
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                                                                   Halluin, Albert
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2001 Ferry Building
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VENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
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Dawson, William O.
Grantham, George L.
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Pred. No. 9.9;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UJETILING DATE: 07-JUNE-PRIOR APPLICATION DATA: APPLICATION NUMBER: UJETILING DATE: 19-JAN-1
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APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 3
FILING DATE: 17-FEB-1989
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APPLICATION NUMBER: 1
FILING DATE: 22-OCT-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                              FILING DATE: 26-FEB-1988 PRIOR APPLICATION DATA:
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                                                PRIOR APPLICATION DATA:
                                                                             FILING DATE: 05-MAY-PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER: US 2 FILING DATE: 15-JUL-1988 ATTORNEY/AGENT INFORMATION:
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TYPE: a
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Turpen, Thomas H
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                                                                   08-JUN-1989
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80.0%;
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                                us 219,279
                                                                               US 363,138
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 Mismatches

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Pred. No. 9
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TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Innear
MOLECULE TYPE: protein
US-08-482-920-6
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US-08-484-341-6
US-08-484-341-6
; Sequence 6, Application US/08484341
; GENERAL INFORMATION:
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Best Local :
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TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PEAtent in Release #1.0, Ve

CURRENT APPLICATION DATA: US/08/484,341

FILING DATE: 07-UN-1995

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Halluin, Albert P. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Donson, Jon
Dawson, William 0.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 CRDD-PYGDG 163
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          PELICATION NUMBER: 08/184,237

FILING DATE: CUNKNOWN

APPLICATION NUMBER: 05 600,244

FILING DATE: 22-OCT-1990

APPLICATION NUMBER: US 641,617

FILING DATE: 22-OCT-1990

APPLICATION NUMBER: US 310,881

FILING DATE: 17-FEB-1989

APPLICATION NUMBER: US 160,766

FILING DATE: 26-FEB-1988

APPLICATION NUMBER: US 347,637

FILING DATE: 26-FEB-1988

APPLICATION NUMBER: US 363,738

FILING DATE: 05-MAY-1989

APPLICATION NUMBER: US 363,138

FILING DATE: 08-JUN-1989

APPLICATION NUMBER: US 363,138

FILING DATE: 08-JUN-1989

APPLICATION NUMBER: US 363,138

FILING DATE: 08-JUN-1989

FILING DATE: 15-UL-1988

FILING DATE: 15-UL-1988
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Similarity 80.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2001 Ferry Building CITY: San Francisco STATE: CAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grantham, George
Turpen, Thomas H.
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 434;
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; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-484-341-6
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: INDEPTATION
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
SOFTWARE: PATCH TON
CLASSIFICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION NUMBER: US/08/483,502
FILING DATE: FLING DATE: US 600,244
FILING DATE: 20-COT-1990
PRIOR APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION NUMBER: US 641,617
FILING DATE: 10-FBB-1989
PRIOR APPLICATION NUMBER: US 310,881
FILING DATE: 26-FEB-1988
PRIOR APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION NUMBER: US 160,771
APPLICATION NUMBER: US 160,771
APPLICATION NUMBER: US 347,637
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: US-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: US-MAY-1989
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Patent No.
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Matches
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APPLICANT: Donson
APPLICANT: Dawson
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TELEPHONE: 415-433-4150
TELEPAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Thomas H.
APPLICANT: Garger, Stephen J.
APPLICANT: Garger, Stephen J.
APPLICANT: Grantham F. Stephen J.
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ZIP: 20005
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 1
FILING DATE: 08-JUNPRIOR APPLICATION DATA:
APPLICATION NUMBER: 1

UMBER: US 363,138 08-JUN-1989

us 219,279

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APPLICANT: DANSON, William O.
APPLICANT: DANSON, William O.
APPLICANT: GRANTHAM, GEORGE L.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Ann M.
APPLICANT: GRARGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
FILE REFERENCE: 008010023CNUS01
CURRENT APPLICATION NUMBER: US/09/726,651A
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Applic Patent No. 6448046
                                                                                                                                                                                                                                          SEQ ID NO 6
                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 07/737,899 PRIOR FILING DATE: 1991-07-26
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 434 amino acids
                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/184,237
                                                                                                                         FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                       ENGTH: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 CRDD-PYGDG 163
                                     Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09726651A
                                       Conservative
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                                                                                                                                              CLONE: alpha-amylase
                                                                                                                               protein
                                                    68.0%;
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                                     0;
                                   Score 41.5; D
Pred. No. 9.9;
0; Mismatches
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Pred. No. 9.9;
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                                     Gaps
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RESULT 13
US-09-072-917A-9
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Best Local Similarity
Thes 7; Conserve
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US-09-252-991A-24086
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US-09-252-991A-31890
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                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 24086
LENGTH: 384
                                                      Sequence 9, Application US/09072917A Patent No. 6288302
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                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
GENERAL INFORMATION:
APPLICANT: Yu, Su
APPLICANT: Liu, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27.
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0 NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                         Local Similarity tes 7; Conserv
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                                                                                                                                                                                                                                           Conservative
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                    Yu, Su-May
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S: 33142
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1998-02-18
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70.0%;
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                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                            Score 38;
Pred. No.
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Pred. No. 14;
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В
                                           ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-19739
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US-09-252-991A-19739
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                                                                                                                                                                                                                                                                                                                   Sequence 19739, Application US/09252991A

Patent NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
                                                                                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 19739
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.3%;
Best Local Similarity 60.0%;
Matches 6; Conservative
Query Match
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/3425
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: bubuc
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 CSDDTQYSDG 157
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: United States of America
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 amino acids
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62.3%;
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Pred. No.
Score 38;
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DB 4;
Length 500;
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FILING DATE: 30-Sep-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/5225-1489
TELEPHONE: 650/522-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUERCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-720-484A-5
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US-08-953-823A-5
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US-08-720-484A-5
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                                                                                                                                                                                                          Sequence 5,
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Best Local :
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                                                                      APPLICANT: DeSauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: ADBLICATION NUMBER: US/08/720.4844
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MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                               / Match 62.3%;
Local Similarity 66.7%;
hes 6; Conservative
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ZIP: 94080
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                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 CRHPRPRADG 349
                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                   68 RDDKPWFDG 76
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                                                        Genentech, Inc
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                                                                                          Vertebrate Smoothened Proteins 5
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0; Mismatches
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Pred. No. 1e+02;
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-398-239-5
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                                                                              RESULT 18
US-09-560-876A-5
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Best Local S
Matches 6
             Sequence 5, Application US/09560876A
Patent No. 6492139
GENERAL INFORMATION:
APPLICANT: de Sauvage, Frederic
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09398239 Patent No. 6407216
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Vertebrate Smoothened Proteins FILE REFERENCE: P1050D1
CURRENT APPLICATION NUMBER: US/09/398,239
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: US 08/720,484
EARLIER FILING DATE: 1996-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosenthal, An APPLICANT: Stone, Donna
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DeSauvage, Frederic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/027070 FILING DATE: 30-Sep-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/953,823A FILING DATE: 30-Sep-1997 CLASSIFICATION: 424
                                                                                                                                                                                                           Local Similarity
nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                             89
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de Sauvage,
Rosenthal,
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66.7%;
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                                                                                                                                                                                                                        Score 38;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                          DB 4;
1e+02;
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1e+02;
                                                                                                                                                                                                                                       Length 1036;
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                                                                                                                                                                                                           Indels
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RESULT 20
US-09-328-352-7068
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                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: unknown amino acid US-09-560-876A-6
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US-09-560-876A-6
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: de Sauvage,
APPLICANT: Rosenthal,
APPLICANT: Stone, Donr
                                                                                                                                             Sequence 7068, App
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09560876A Patent No. 6492139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/560,876A CURRENT FILING DATE: 2002-05-22 PRIOR APPLICATION NUMBER: US 60/027,070 PRIOR FILING DATE: 1996-09-30 PRIOR APPLICATION NUMBER: US 08/953,823 PRIOR FILING DATE: 1997-09-30 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/560,876A CURRENT FILING DATE: 2002-05-22 PRIOR APPLICATION NUMBER: US 60/027,070 PRIOR FILING DATE: 1996-09-30 PRIOR APPLICATION NUMBER: US 08/953,823 PRIOR FILING DATE: 1997-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothened Proteins
FILE REFERENCE: P1050R1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P1050R1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stone, Donna TITLE OF INVENTION: Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1036
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure LOCATION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 6; Conserv
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                                                                                                                                                                Application US/09328352
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66.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               Score 38; DB 4;
Pred. No. 1.1e+02;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION UNMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22461
LENGTH: 568
TEURING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
US-08-991-862-17
; Sequence 17, Application US/08991862
; Patent No. 6309826
; Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
US-09-252-991A-22461
; Sequence 22461, Ap
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-08-991-862-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Acinetobacter baumannii US-09-328-352-7068
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Best Local S
Matches 8
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APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: Z9996.488/P001-A
CURRENT APPLICATION NUMBER: U5/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTINOS: 17
LENGTH: 593
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22461, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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LENGTH: 217
                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
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Local Similarity 77.8%;
es 7; Conservative
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Local Similarity 50.0%;
es 8; Conservative
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185 RDDRRYYDG 193
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211 CRADRPRAAG 220
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                               1 CRDDRPYADG 10
                                                                  Similarity 70. 7; Conservative
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70.0%;
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Pred. No.
                                                                                   Score 36; DB 4; Length 568; Pred. No. 1.2e+02;
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                                                                      Mismatches
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RESULT 23
US-09-216-393B-62
; Sequence 62, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES
; FILE REFERENCE: TX-1-C2
; FILE REFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08;
Patent No. 6015702
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jenni
APPLICANT: Corley, Neil C
TITLE OF INVENTION: HUMAN
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US-08-965-689A-6
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
LENGTH: 129
TYPE: PRT
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,689A |
FILING DATE: Herewith
CLASSIFICATION LATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION OMERE: 08/933,750
APPLICATION NUMBER: 08/933,750
APPLICATION HOMBER: 08/933,750
APPLICATION NUMBER: 35,149
APPLICATION UNUMBER: 36,749
APPLICATION UNUMBER: 36,749
APPLICATION UNUMBER: 36,749
APPLICATION UNUMBER: 36,749
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Best Local :
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           INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 165 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Toxoplasma
                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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nes 6; Conserv
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CRDERELASG 121
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o. 6015702
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60.0%;
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Pred. No. 40;
1; Mismatches
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; Sequence 6, Application US/09359967; Patent NO. 6146624; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L. APPLICANT: Corley, Neil C. APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN UBIQUIT NUMBER OF SEQUENCES: 6
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US-08-965-689A-6
В
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Best Local S
                                                                    Query Match
Best Local :
                                                        Matches
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IMMEDIATE SOURCE:
LIBRARY: GenBar
TONE: 4257
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 23, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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SOFTWARE: FastSEC
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                          4 DRPYADG 10
                                                     Similarity
6; Conserva
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                                                                                                                                                                                                              165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc. 
3174 Porter Drive
                                                                                                                                        GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
52
                                                                                                                                                                                   single
                                                                    57.4%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN UBIQUITIN CONJUGATING ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
85.7%;
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                                                                                                                                                                                                                                                                                                                  PF-0356-1 CIP
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                                                       0;
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Pred. No.
                                                                    Score 35; DB 3; Length 165; Pred. No. 52;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-484-905-75
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US-08-484-905-75
                                                                                                                                                                                                         RESULT 27
                                                                                                                                                                                            US-08-481-985B-75
                                                                                                                          Sequence 75, Application US/08481985B Patent No. 6011146 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08, FILING DATE: 07-JUNE-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                 APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 148 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 15-NOV-1991 CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow,
                                                                                                                                                                                                                                                                       155 RDDRAYLEG 163
                                                                                                                                                                                                                                                                                                         2 RDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5, Application US/08484905 5976551
                                                                                                                                                                                                                                                                                                                                            Similarity 66. 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202-408-4400
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                              DB;
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TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENCTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
US-08-370-476-75
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Best Local S
Matches 6
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Patent No. (
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ZIP: 2005-3315

ZIP: 2005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, \

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Mottez
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CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/801,818
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
FILING DATE: 435
                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                               TITLE OF INVENTION: Altered Major Histoco
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATE: 05 07/792,473
PRIOR DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                            APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armanda
APPLICANT: Casrouge, Armanda
APPLICANT: Casrouge, Armanda
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                                                                                  STATE: D.C.
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 57.4%;
Local Similarity 66.7%;
hes 6; Conservative
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/481,985B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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155 RDDRAYLEG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RDDRPYADG 10
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                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                       Mottez, Estelle
                                                                                                                                                                                     Finnegan, Henderson, Farabow, Garrett &
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Version #1.25
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CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SED ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 362
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-84
RESULT 30
US-09-252-991A-18424
; Sequence 18424, Application US/09252991A
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US-08-846-762-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4000
TINFORMATION FOR SEQ ID NO: 7.
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linea-
NOLECULE TIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. GENERAL IN
                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
EILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
PILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/370,476
                                                                                     341 RDVQPYGDG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84, Application US/08846762A
o. 5994072
                                                                                                                     2 RDDRPYADG 10
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                                                                                                                                                      Similarity 6; Conserv
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                                                                                                                                                        Conservative
                                                                                                                                                                    57.4%;
66.7%;
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66.78;
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ER: 05243.0001-01000
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Pred. No. 1.2e+02;
1; Mismatches 2;
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Pred. No. 98;
1; Mismatches
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                                                                                                                                                                                        Length 362;
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                                                                                                                                                        Indels
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; Patent No. 6551795;
; GENERAL IMFORMATION:
; APPLICANT: MAIC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; FILE OF SEQ ID NOS: 33142
; TYDE: PRI
US-09-252-991A-18424
US-09-252-991A-18424
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Search completed: August 29, 2003, 18:44:40 Job time: 11.5714 secs
                                                                                                 В
                                                                                                                                                                                      Query Match 57.4%; Score 35; DB 4; Length 444; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                          3 DDRPYA 8
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198 DDRPYA 203
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Title: Perfect score: Sequence:

Scoring table:

Database

Run

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protein 90.

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 100:
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                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                    Published_Applications_Aa:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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Sequence 40, Appl
Sequence 111, Appl
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 Sequence 59, Appli Sequence 21, Appli Sequence 2, Appli Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1093; A ppli Sequence 1093; A ppli Sequence 1026; A ppli Sequence 200, Appli Sequence 62, Appli Sequence 11224, A sequence 11224, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11719, A Sequence 11717, Appli Sequence 11717, Appli Sequence 11717, Appli Sequence 11717, Appli Sequence 11717, Appli Sequence 11717, Appli Sequence 11717, Appli Sequence 11847, Appli Sequence 11847, Appli Sequence 11847, Appli Sequence 11820, Appli Sequence 11820, Appli Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A Sequence 11820, A
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Result No.

Score

112110

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RESULT 2
US-10-156-761-8392
; Sequence 8392, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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US-10-280-679B-6
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PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR APPLICATION NUMBER: 07/737,899
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Best Local
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     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/310,881 PRIOR FILING DATE: 1999-02-17 PRIOR APPLICATION NUMBER: 07/160,766 PRIOR FILING DATE: 1998-02-26 PRIOR APPLICATION NUMBER: 07/160,771 PRIOR FILING DATE: 1988-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/557,941
PRIOR FILING DATE: 2000-04-24
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PRIOR APPLICATION NUMBER: 07/739,143
PRIOR FILING DATE: 1991-08-01
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ORGANISM: Rice alpha-amylase
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US-09-946-374-324

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US-10-006-130A-324

US-10-199-672-354

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US-09-815-242-13417
US-09-815-242-13569
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US-09-815-242-13842
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Sequence 13417, A
Sequence 13569, A
Sequence 6, Appli
Sequence 324, App
Sequence 324, App
Sequence 324, App
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Sequence 334, App
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13842, A
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHABA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-07
PRIOR FILING DATE: 2001-08-02
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SEQ ID NO 8392
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US-10-155-886-11
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APPLICANT: Lee, Ramee
APPLICANT: Teng, Kenneth K.
APPLICANT: Kermani, Pouneh
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
CURRENT APPLICATION NUMBER: US/10/155,886
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 118
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/10155886 Publication No. US20030087804A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                       Sequence 11, Application US/10155886 Publication No. US20030087804A1
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Best Local Similarity
Matches 6; Conserv
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Best Local :
APPLICANT: Hempstead, Barbara L.
APPLICANT: Lee, Ramee
APPLICANT: Teng, Kenneth K.
APPLICANT: Kermani, Pouneh
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REFERENCE: 955-21 Sequence No. US:20030087804A1. 1-68
CURRENT APPLICATION NUMBER: US:/10/155,886
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
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66.7%;
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Pred. No. 1.2e
1; Mismatches

    Mismatches

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tches 2;
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; ORGANISM: Gallus gallus
US-10-155-886-11
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US-10-097-340-141
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RESULT 6
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Best Local S
Matches 7
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LENGTH: :
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 413
TYPE: PRT
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-08-10
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PRIOR FILING DATE: 2001-09-19
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PRIOR FILING DATE: 2001-09-26
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Local Similarity 60.0%;
tes 6; Conservative
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                                                  147 RDYRPYAD 154
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243
                                                                                                                 Similarity
7; Conserv
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Rachel E. MEYERS
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Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karen LU
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C. BAST, Jr.
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Pred. No.
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US-09-824-647-17
Sequence 17, Application US/09824647
Publication No. US20020183270A1
GENERAL INFORMATION:
APPLICATION: Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CUURENY PILING DATE: 2001-04-04
CUURENY PILING DATE: EARLIER APPLICATION NUMBER: US/09/824,647
CUURENT FILING DATE: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION UNDER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 593
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US-09-824-807-17
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SEQ ID NO 17
LENGTH: 593
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Best Local Similarity 50...
"Arches 8; Conservative
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Best Local
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TITLE OF INVENTION: 88 KDA TOMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996, 488/D-001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
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APPLICANT: Series, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29956.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-62-23
RIOR FILING DATE: 1997-62-23
RUMBER OF SEQ ID NOS: 17
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Pred. No.
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Pred. No.
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^a 1; Indels
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-10-281-160-17
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JS-10-281-160-17

Sequence 17, Application US/10281160

Publication No. US20030108950A1

GENERAL INFORMATION:
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; ORGANISM: Human GP88 cDNA
US-10-218-509-17
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Best Local
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Best Local
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
Query Match
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                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/281,160 CURRENT FILING DATE: 2002-10-28 PRIOR APPLICATION NUMBER: US/08/991,862 PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                             APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
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PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
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8; Conserv
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8; Conserv
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
 Score 37;
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 15;
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Length 593;
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Query Match
Best Local Similarity
Watches 5; Conserve
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                                                                              ; TYPE: PRT; ORGANISM: homo sapiens US-09-784-358-12
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US-09-784-358-12
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Query Match
Best Local Similarity
"~+~hes 5; Conserve
                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Donoho,
APPLICANT: Scovill
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                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09784358 Patent No. US20020099027A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09784358 Patent No. US20020099027A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/784,358
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,282
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/784,358
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,282
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                               APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
TITLE OF INVENTION: POLYNICLEOTIDES ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sands, Arthur T
TITLE OF INVENTION: NOLL HUMAN THROMBOSPONDIN REPEAT PROTEINS
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0134-USA
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                 FILE REFERENCE: LEX-0134-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                LENGTH: 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 CRDEKPHA 676
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Turner, C. Alexander Jr.
Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                     Turner, C. Alexander Jr. Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                   Zambrowicz, Brian
                                                                                                                                                                                                                                                                                                                                                                                       Scoville,
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62.5%;
                               60.7%;
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1; Mismatches 1;
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                 Mismatches
                             Score 37; DB 9;
Pred. No. 2e+02;
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                                                DB 9;
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                                                Length 845;
                 Indels
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Length 1023;

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APPLICANT: Shinkels, Richard A
APPLICANT: Shinkels, Steven K
APPLICANT: Spaderna, Steven K
ITILE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
CURRENT APPLICATION NUMBER: US/09/789,390
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185,548
PRIOR TILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/199,957
PRIOR APPLICATION NUMBER: 60/194,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/187,723
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION UNMER: US/09/789,390
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION UNMERE: 60/185,548
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION UNMER: 60/184,951
PRIOR APPLICATION UNMER: 60/185,967
PRIOR APPLICATION UNMER: 60/185,967
PRIOR APPLICATION UNMER: 60/187,723
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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; ORGANISM: Homo sapiens
US-09-789-390-25
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US-09-789-390-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Applica Publication No. US20 GENERAL INFORMATION:
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APPLICANT: Fernandes, Elma
APPLICANT: MacDougall, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: MacDougall, John
APPLICANT: Shimkets, Richard
APPLICANT: Spaderna, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shimkets, Richard A
APPLICANT: Spaderna, Steven K
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ication No
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743 CRDEKPHA 750
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No. US20030059768A1
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CURRENT APPLICATION NUMBER: US/09/789,390
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185,548
PRIOR APPLICATION NUMBER: 60/185,548
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/199,957
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR APPLICATION NUMBER: 60/184,951
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/187,723
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/197,723
PRIOR APPLICATION NUMBER: 60/197,723
PRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 77
SEO ID NO 28
LENGTH: 1023
TYPE: PRT
ORGANISM: HOMO Sapiens
US-09-789-390-28
   Sequence 59, Application US/09789390
Publication No. US20030059768A1
GENERAL IMFORMATION:
APPLICANT: Fernandes, Elma
APPLICANT: MacDougall, John
APPLICANT: Shimkets, Richard A
APPLICANT: Spaderia, Steven K
APPLICANT: Spaderia, Steven K
INTEL OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
CURRENT APPLICATION NUMBER: 0001-02-23
PRIOR APPLICATION NUMBER: 5001-02-23
PRIOR APPLICATION NUMBER: 607185,548
PRIOR APPLICATION NUMBER: 607185,548
PRIOR APPLICATION NUMBER: 607199,957
PRIOR FILING DATE: 2000-04-27
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US-09-789-390-59
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US-09-789-390-28
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publication No. US20030059768A1
GEMERAL INFORMATION:
APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
APPLICANT: MacDougall, John
APPLICANT: Minkets, Richard A
APPLICANT: Spidmets, Richard A
APPLICANT: Spidmets, Richard A
APPLICANT: Spidmets, Richard A
APPLICANT: Spidmets, Richard A
APPLICANT: Spidmets, Richard A
APPLICANT: Spidmets, ROYEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
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Best Local S
Matches 5
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Best Local Similarity 62.9
Matches 5; Conservative
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TYPE: PRT
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Local Similarity 62.5%;
les 5; Conservative
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Pred. No. 2.4e+02;
3; Mismatches 0;
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cches 0;
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US-09-789-390-2
; Sequence 2, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
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US-09-789-390-61
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                                                                                                                                                 RESULT 18
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PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/185,967
PRIOR APPLICATION NUMBER: 60/185,967
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/197,723
PRIOR FILING DATE: 2000-04-18
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Matches
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LENGTH: 1023
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fernandes, Elma
APPLICANT: MacDougall, John
APPLICANT: Shimkets, Richard A
APPLICANT: Spaderna, Steven K
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/197,723
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 77
                 APPLICANT: Vernet, Corine APPLICANT: Fernandes, Ell APPLICANT: MacDougall, J
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                                                                                                                                                                                                                                                                        Local Similarity
nes 5; Conserv
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                                                                                                                                                                                                      CRDEKPHA 82
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Fernandes, Elma
MacDougall, John
Shimkets, Richard A
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62.5%;
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Pred. No.
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Вb
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US-09-789-390-5
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                                                                                                                                                                                                                                       SEQ ID NO 5
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                                                                             Matches
                                                                                                                  Query Match
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APPLICANT: Spaderna, Steven K
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
CURRENT APPLICATION NUMBER: US/09/789,390
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185,548
PRIOR APPLICATION NUMBER: 60/185,548
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/185,967
PRIOR FILING DATE: 2000-03-01
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APPLICANT: Fernand
APPLICANT: MacDoug
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PRIOR FILING DATE: 2000-04-27
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TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-692
                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS
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NUMBER OF SEQ ID NOS: 77
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TYPE: PRT
                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                    LENGTH: 1281
TYPE: PRT
                                                                                                  Local
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                                                                             Similarity
5; Conserv
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MacDougall, John
                                                                               Conservative
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NOS: 77
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                                                                                                  60.7%;
                                                                               Score 37; DB 11;
Pred. No. 3.1e+02;
3; Mismatches 0;
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Pred. No. 3.1e+02;
3; Mismatches 0;
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APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0134-USA
CURRENT APPLICATION NUMBER: US/09/784,358
CURRENT FILING DATE: 2001-02-17
INUMBER OF SED IN NOS: 17
SOFTWARE: PASTSEQ for Windows Version 4.0
SED ID NO 16
LENGTH: 1617
RESULT 22
US-09-789-390-4
; Sequence 4, Application US/09789390
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; ORGANISM: homo sapiens
US-09-784-358-2
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; ORGANISM: homo sapiens
US-09-784-358-16
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THE SAME
FILE REFERENCE: LEX-0134-USA
CURRENT APPLICATION UNMERS: US/09/784,358
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION UNMERS: US 60/183,282
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 17
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1691
TYDE: DATE: 1891
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Best Local S
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Patent No. US20020099027A1
GENERAL INFORMATION:
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Best Local :
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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Local Similarity 62.5%;
es 5; Conservative
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Local Similarity 62.5%;
es 5; Conservative
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20020099027A1
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3.9e+02;
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PRIOR APPLICATION NUMBER: 60/185,548
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/185,967
PRIOR APPLICATION NUMBER: 60/197,723
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 77
SEQ ID NO 4
LENGTH: 1691
TYPE: PRT
ORGANISM: Homo sapiens
US-09-789-390-4
                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT EILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/216,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-10-21
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-10-11
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Best Local S
Matches 5
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APPLICANT: Carr,
APPLICANT: Yaman
APPLICANT: Xu, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Ichn
APPLICANT: MacDougall, John
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Spaderna, Steven K
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/789,390
CURRENT FILING DATE: 2001-02-23
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Local Similarity 62.5%;
les 5; Conservative
NO 10983
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o. US20020061569A1
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                   FastSEQ for Windows Version 4.0
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Yamamoto, Robert T.
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Pred. No. 4.1e+02
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PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10261

LENGTH: 255
                                                           US-09-815-242-14085
, Sequence 14085, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
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; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-10983
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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Best Local (
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITAA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 CURRENT FILING DATE: 2001-03-21
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                 APPLICANT:
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                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                   3 DDRPYADG 10
                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDRPYADG 10
                                                                                                                                                                                                  DDRPYGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDRPYGGG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck,
               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                    Conservative
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75.0%;
                                                                                                                                                                                                                                                                                  59.0%;
75.0%;
                                                                                                                                                                                                                                                                  Score 36; DB Pred. No. 88; 0; Mismatches
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                                                                                                                                                                                                                                                                                                  9;
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                                                                                                                                                                                                                                                                                                Length 255;
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US-10-156-761-7849
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                                                                                                                        ; ORGANISM: Streptomyces avermitilis US-10-156-761-7849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Salmonella typhi
US-09-815-242-14085
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14085
                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local
                                         Matches
                                                            Query Match
Best Local
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CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 DDRPYGGG 57
  2 RDDRPY 7
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                                         6;
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%;
75.0%;
                                                            59.0%;
100.0%;
                                         Score 36; DB ;; Pred. No. 1.2 0; Mismatches
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Pred. No.
                                         DB 15; I
. 1.2e+02;
ches 0;
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                                                                                Length 353;
                                           Indels
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                                         Gaps
                                         0;
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264 RDDRPY 269

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RESULT 27
US-10-097-534-27
; Sequence 27, Application of US20030; Publication No. US20030; Publication GREENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORRENER, TORR
                                                          APPLICANT: KACCUMMANNIAN APPLICANT: VA, GUO-Liang
APPLICANT: VA, GUO-Liang
APPLICANT: Pineda, Omaira
TITIE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MB1-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT APPLICATION NUMBER: 05/27439
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR FILING DATE: 2001-41-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 200
LENGTH: 280
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; SEO ID NO 27
; LENGTH: 4834
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-534-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GREENER, TSVIKA
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: MASSOWITZ, HAIM
APPLICANT: ALROY, IRIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
FILE REFERENCE: PLV-001.01
CURRENT APPLICATION NUMBER: US/10/097,534
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,224
PRIOR APPLICATION NUMBER: 60/308,958
PRIOR APPLICATION NUMBER: 60/308,958
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
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US-09-934-455-200
LENGTH: 280
TYPE: PRT
CRGANIAN: Arabidopsis thaliana
US-09-934-455-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.0%;
Local Similarity 50.0%;
es 5; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Creelman, Robert
Dubell, Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10097534
No. US20030049607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reuber, Lynne
Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09934455
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APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: FAICO, S. Carl

TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLYLTRANSFERASE
FILE REFERENCE: BB1419 US NA
CURRENT APPLICATION NUMBER: US/10/233,926
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US/09/735,846
PRIOR APPLICATION NUMBER: US/09/735,846
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 328
TYPE: PRT
ORGANISM: Zea mays
US-10-233-926-14
                                                                       DЬ
                                                                                                                                                                                                                 ; ORGANISM: Toxoplasma gondii US-09-216-393-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-216-393-62
Sequence 62. Application US/09216393
Patent No. US20010014447A1
GENERAL INFORMATION:
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US-10-233-926-14
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Search completed: August 29, 2003, 18:47:47 Job time: 17.7143 secs
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                       APPLICATE MILHAUSEN, MICHAEL James
APPLICATE OF INVENTION: TOXOPLASMA GONDII PROTBINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT FILING DATE: 1998-12-18
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 62
LENGTH: 129
TYPE: PRI
COCCANTENT TOXOCLERMS GOOGLE
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Best Local Similarity /2...
Conservative
Conservative
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                                                                                                                                           Matches
                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/10233926 Publication No. US20030131382A1
                                                                                                                                         Local Similarity 60.0es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 CNDDFTPYVDG 204
                                                                       112 CRDERELASG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 DDRPVRVYADG 82
                                                                                                        1 CRDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRDD-RPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DDRP---YADG 10
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72.7%;
                                                                                                                                                         57.48;
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0; Mismatches
                                                                                                                                         Score 35; DB 9; Length 129; Pred. No. 66; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.5; DB 16
Pred. No. 1.4e+02;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 280; .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
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Result No.

ALIGNMENTS

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alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2 C;Species: Hordeum vulgare (barley) C;Date: 30-un-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999 C;Accession: A31960; A00847; JE0405; A26267; A24457; A30759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed by the embryo during germination.
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position:
A;Map position:
A;Introns: 29/3; 344/3
A;Introns: 29/3; 344/3
A;Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-amyC;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt. A;Reference number: A24457
A;Reference number: A24457
A;Accession: A24457
A;Molecule type: protein
A;Residues: 25-59,'X',61-67,'HX',70-85,'X',87-92,'E',94;146-165;228-251;297-303,'X',C;Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulate ed by the embryo during germination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-133, 'V',135-184, 'A',186-366, 'GA' <CHA>
A; Residues: 1-33, 'V',135-184, 'A',186-366, 'GA' <CHA>
A; Experimental source: cv. Himalaya
A; Note: the authors translated the codon GTC for residue 134 as (R; Svensson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.
Carlsberg Res. Commun. 50, 15-22, 1995
Carlsberg Res. Commun. 50, 15-22, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-133,'D',',135-424,'Q',426-427 <RAH>
A;Residues: 1-133,'D',135-424,'Q',426-427 <RAH>
A;Cross-references: EMBL:X15226; NID:g18894; PIDN:CAA33298.1; PID:g295804
A;Experimental source: gene Amy152
R;Chandler, P.M.; Zwar, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Inglis, A.S.
Plant Mol. Biol. 3, 407-418, 1984
A;Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels
A;Reference number: A26267
A;Accession: A26267
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A;Title: Nucleotide and predicted amino acid sequences of two different genes for high-pa;Reference number: JE04405
A;Reference number: JE04405
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J. Biol. Chem. 260, 3731-3738, 1985

A;Title: Two barley alpha-amylase gene families are regulated differently in A;Reference number: A00847; MUID:85131184; PMID:3871776

A;Accession: A00847
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A; Residues: 1-427 < KHU>
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A;Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA level
A;Reference number: A92700; MUID:89066691; PMID:3264283
A;Accession: A31960
                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: aleurone cell; blocked amino end; calcium binding; germination; glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-133,'D',135-194,'HRL',198-424,'Q',426-427 <ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: cv. Himalaya; gene Amy6-4
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                                                                                                                                                  F;25-427/Product: alpha-amylase #status experimental <MAT>
F;170-316/Domain: alpha-amylase core homology <AMY>
F;25/Modified site: blocked amino end (Gln) (in mature form)
F;203,228,313/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rogers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:J04202
                                                                                                                                                                                                                                                               F;1-24/Domain: signal sequence *status predicted <SIG> F;25-427/Product: alpha-amylase *status experimental <
           Matches
                                                                           Query Match
                                         Local
                                     Similarity
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                                 100.0%;
           0
           Pred. No. 0. Mismatches
                                                                       Score 61;
                                 No.
. 0.0011;
                                                                                  DB
                                                                           Length 427;
                                                                                                                                                                                    (probably pyrrolidone
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           0;
           Gaps
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unstimulated al
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                                                                       C; Function:
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                                                                                                                                                                                                                                                                       A; Gene:
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R;Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S. J. Mol. Appl. Genet. 2, 579-588, 1984
A;Reference number: A92837; MUID:85159405; PMID:6335720
A;Accession: B21826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Hordeum vulgare (barley) C;Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999 C;Accession: JE0406; B30759; S06275; B31960; B21826 R;Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrish Plant Mol. Biol. 12, 119-121, 1989 A;Title: Nucleotide and predicted amino acid sequences of two different genes for hig A;Reference number: JE0405
                                                                                                                                                                                                                                                                                                                                                                                       A;ACCESSION. ----
A;Molecule type: mRNA
A;Residues: 379-389,'T',391-392,'D',394-429 <HUA>
A;Residues: 379-389,'T',391-392,'D',394-429 <HUA>
A;Cross-references: GB:K02636; NID:g166992; PIDN:AAA32932.1; PID:g166993
A;Cross-references: GB:K02636; NID:g166992; PIDN:AAA32932.1; PID:g166993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 263, 18953-18960, 1988
A;Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA
A;Reference number: A92700; MUID:89066691; PMID:3264283
A;Accession: B31960
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA A;Molecule type: DNA A;No. 156-160, 'PD', 163, 'G', 167-196, 'V', 198-342, 'T', 344-39 A;Residues: 1-104, 'G', 106-154, 'A', 156-160, 'PD', 163, 'G', 167-196, 'V', 198-342, 'T', 344-39 A;Cross-references: GB:,704202; NID:g166984; PIDN:,AAA98615.1; PID:g166985 A;Experimental_source: cv. Himalaya gene Amy46 for alpha-amylase B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-11, 'LI', 14-32, 'S', 34-57, 'I', 59-79, 'Y', 81-139, 'R', 141-160, 'PA', 163-164, 'A; Residues: 1-11, 'LI', 14-32, 'S', 34-57, 'I', 59-79, 'Y', 81-139, 'R', 141-160, 'PA', 163-164, 'A; Cross-references: EMBL:M17125; NID:9166978; PIDN:AAA32926.1; PID:9166979
A; Experimental source: CV. Sundance gene for alpha-amylase 1 precursor (clone p141.11
A; Genetics: AA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, Plant Mol. Biol. 9, 3-17, 1987
A;Title: Structure and organization of two divergent alpha-amy A;Reference number: S06275
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A;Experimental_source: gene Amy56 for alpha-amylase
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-51 <KHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Khursheed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
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A; Residues: 1-429 < RAH>
                                                                                                                 A; Introns: 29/3;
                                                                                                                                                   A; Map position: 6
                                                                                                                                                                                                                               C; Genetics: <AAl>
                                                                                                                                                                                                                                                                                                           C; Genetics: <A46>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Rogers, J.C.
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                                                                                                                                                                                                                                                                     Amy46
                                                                                                                                                                                                                                                                                                                                                                               Amy56
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A94535
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 24-31 <YAN>
R; Takeuchi, H; Yamauchi, D.; Wada, S.; Minamikawa, T.
submitted to the EMBL Data Library, June 1993
A; Description: Nucleotide sequence of the alpha-amylase gene from A; Reference number: $40201
A; Reference number: $40201
A; Accession: $40201
A; Molecule type: DNA
A; Residues: 1-421 <TAK>
A; Residues: 1-421 <TAK>
A; Cross-references: EMBL:X73301; NID:9437944; PIDN:CAA51734.1; PID C; Genetics: 38/3; 72/1; 340/3
C; Function: Cstallwee the budgeling of internal 1 4-21ch-1-22.
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$10514
alpha-amylase (EC 3.2.1.1) precursor - black gram
C; Species: Vigna mungo (black gram)
C; Species: Vigna mungo (black gram)
C; Bate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Accession: $10514; $61336; $40201; $61334
R; Yamauchi, D.; Minamikawa, T.
Nuclecias Res. 18, 4250, 1990
A; Title: Nucleotide sequence of cDNA for alpha-amylase from cotyledons of gath, Reference number: $10514; MUID:90332425; PMID:2377468
alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley c; Species: Hordeum vulgare (barley) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change C;Accession: S07040 R;Knox, C.A.P; Sonthayanon, B; Chandra, G.R.; Muthukrishnan, Plant Mol. Biol. 9, 3-17, 1987 A;Title: Structure and organization of two divergent alpha-amyl A;Reference number: S06275 A;Accession: S07040 A;Molecule type: DNA A;Residues: 1-437 <KNO>
                                                                                                                                                                                                                                                               RESULT 4
S07040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: catalyzes the hydrolysis of internal 1.4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
F;1-32/Domain: signal sequence #status predicted <SIG>
F;24-421/Product: alpha-amylase #status experimental <MAT>
F;261-312/Domain: alpha-amylase #status experimental <MAT>
F;201,226,309/Active site: Asp, Glu, Asp #status predicted
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A; Molecule type: mRi
A; Residues: 1-421 <
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Best Local S
Matches 9
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Best Local S
Matches 7
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9; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                          28-Feb-1990 #text_change
                                                                                                divergent alpha-amylase
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0.0098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g437945
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RESULT 6
$10013
$10013
$10013
alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2) - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
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C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
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C;Accession: $10013 *sequence_revision 17-Nov-1995 *text_change 22-Jun-1999
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C;Accession: $10013 *text_change 22-Jun-1999
C;Accession: $10013 *text_change 22-Jun-1999
C;Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-amylase (EC 3.2.1.1) precursor - barley
c;Species: Hordeum vulgare (barley)
c;Species: Hordeum vulgare (barley)
c;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999
c;Accession: A00846; S65602
C;Accession: A00846; S65602
A;Richie: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
A;Reference number: A00846; MUID:83238423; PMID:6190808
A;Accession: A00846
A;Molecule type: mRNA
A;Residues: 1-438 <ROG>
A;Residues: 1-438 <ROG>
A;Residues: 1-438 <ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987 A;Experimental source: cv. Himalaya A;Experimental source: cv. Himalaya R:Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B. FEBS Lett. 363, 299-303, 1995
A;Title: Isozyme hybrids within the protruding third loop domain of the la;Reference number: S65602; MUID:95255567; PMID:7737421
A;Accession: S65602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 25-29 < JUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Comment: Production of this enzyme in barley is hormonally regulated.
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Pred. No. 1.8;
1; Mismatches
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Pred. No. 1.8;
1; Mismatches
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RESULT 7
$12775

alpha-amylase (EC 3.2.1.1) precursor (clone pOS103) - rice C:Species: Oryza sativa (rice) C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_c) C:Accession: $12775
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                                                                                                                                                                                                                                             hypothetical protein 151 - Rhizobium meliloti
c;Species: Rhizobium meliloti
c;Species: Rhizobium meliloti
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Oct-1999
C;Accession: S04123; S32840; S39987
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A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and A;Reference number: S12775; MUID:90318322; PMID:2370848
A;Accession: S12775
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A; Residues: 1-428 <HUA>
A;Cross-references: EMBL:X1
R;Kahn, D.D.
submitted to the EMBL Data
A;Reference number: S32837
A;Accession: S32840
                                                                                                   EMBO J. 8, 1279-1286, 1989
A;Title: fixK, a gene homologous with for and crp from A;Reference number: S04122; MUID:89305532; PMID:2663474
A;Recession: S04123
A;Molecule type: DNA
A;Residues: 1-151 <BAT>
                                                                                                                                                                                                       R;Batut, J.; Daveran-Mingot, M.L.; David, M.; Jacobs, J.; EMBO J. 8, 1279-1286, 1989
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A; Residues: 1-434 < ONE>
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8; Conserv
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                                                                                EMBL: x15079; NID: g48690; PIDN: CAA33184.1;
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80.0%;
                                        Library, March 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-Sep-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA34516.1; PID:g20167
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                                                                                                                                                                                    Escherichia
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                                                                                  PID:g48692
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                                                                                                                                                                                    coli,
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                                                                                                                                                                                    regulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-151 <KAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-151 < KUR>
                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-278 <YUN>
                                                                                                                                                                                                         A; Accession: T03440
                                                                                                                                                                                                                                                                                                                                                                                               T03440
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SMa1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B95345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 CRDDQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRDDRPY 7
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A;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
R;Gallbert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlo
pela, D; Chain, P.; Cowie, A; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fish
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.;
A;Authors: Kahn, D.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:111474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
""" 6; Conserv?
                                               C;Superfamily: plant chitinase; plant chitinase homology C;Keywords: glycosidase; hydrolase; polysaccharide degra F;54-276/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                          C;Accession: T03440
R;Yun, C.H.; Lee, M.C.; Lee, J.S.; Yun, K.J.; Eun, M.Y.
submitted to the EMBL Data Library, April 1997
A;Description: Isolation and characterization of a rice
A;Reference number: Z14947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: Z21854; NID: g49403; PIDN: CAA79900.1; PID: g49407
                                                                                                                                                                                                                                                                                                                                                                                                                                probable chitinase (EC 3.2.1.14) - rice (fragment)
C; Species: Oryza sativa (rice)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Barnett, M.J.; Fisher, R.F.; Jones, T.; .; Kalman, S.; Keating, D.H.; Palm, C.; Po
                                                                                                                                                    A;Cross-references: EMBL:AF001501; NID:g2109456; PID:g2109457
                                                                                                                                                                                                                                     A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SMa1223 [imported] .
C; Species: Sinorhizobium meliloti
                                                                                                                             A; Experimental source: cv. IR36
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6; Conserv
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85.7%;
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85.7%;
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Pred. No. 2.4;
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                           from
                                                                              polysaccharide degradation
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                                                                                                                                                                                                                                             GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                      24-Mar-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komp, C.; Abola, A.P.; Barloy-Hubler, eck, M.C.; Surzycki, R.; Wells, D.H.; Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sinorhizobium meliloti (strain 1021) magapl
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                                                                                                                                                                                                                                                                                                                              of a rice
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Length 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Wong, K.;
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; Fisher, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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67.28;

Score 41;

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R;Gardner, A.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19857
A;Accession: T24216
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 11469 A; Residues: 1169 FIDN:CAA84669.1; GSPDB:GN
A; Cross-references: EMBL:235602; PIDN:CAA84669.1; GSPDB:GN
A; Experimental source: clone R13610
R; Chuang, P.T.; Albertson, D.G.; Meyer, B.J.
Cell 79, 459-474, 1994
A; Title: DPY-77:a Chromosome condensation protein homolog
A; Title: DPY-77:a Chromosome condensation PMID:7954812
A; Reference number: A55095; MUID:95042743; PMID:7954812
A; Accession: A55995
                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Mosecule type: DNA A;Residues: 1-1132,'G', 1134-1469 <CHU>A;Cross-references: GB:L35274; NID:9529384; PIDN:AAA620A;NOte: authors translated the codon GAT for residue 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome condensation protein homolog DPY-27 - Caenorhabditis elegans W;Alternate names: protein R13G10.1 C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-: C;Accession: T24216; A55095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;165-309/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ramachandiran, S.; Srinivasa, B.; Mahadevan, S.
submitted to the EMBL Data Library, February 1994
s,Description: Molecular Cloning and nucleotide sequence of detachment induced alpha amy
                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: AMY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: Molecular c. A; Reference number: Z16900 A; Accession: T09942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T09942
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lpha-amylase (EC 3.2.1.) precursor - southern Asian dodder (fragment)
;Alternate names: alpha-1,4-glucan-4-glucanchydrolase
;Species: Cuscuta reflexa (southern Asian dodder)
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
Matches
                                                                                                CESP: R13G10.1
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142/3; 176/3; 296/2; 548/2; 627/3; Lly: chromosome segregation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRDDRPYADG 10
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6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 60.0%; 6; Conservative
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                                                                                                                                                       69 <CHU>
NID:g529384; PIDN:AAA62647
codon GAT for residue 1133
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 2; Length 423 Pred. No. 6.6;
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697/2;
SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPDB:GN00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                             847/3; 993/3; 1086/2; 1202/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                              .1;
                                                                                                                                                                                                                                                                                                                                                                                 that
                                                                                                                                                           PID:g529385
Gly
                                                                                                                                                                                                                                                                                                                                                                                 regulates Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CESP: R13G10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                 1383,
                                                                                                                                                                                                                                        A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation c;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;168-31/Domain: alpha-amylase core homology cAMY> F;202,228,314/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-amylase (BC 3.2.1.1) 2A - rice
C;Species: Oryza sativa (rice)
C;Date: 17-Aug-192 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999
C;Date: 17-Aug-192 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999
C;Accession: J01527
R;Huang, N.; Reinl, S.J.; Rodriguez, R.L.
Gene 111, 223-228, 1992
A;Title: RAmy2A; a novel alpha-amylase-encoding gene in rice.
A;Reference number: J01527; MUID:92175526; PMID:1541400
A;Accession: J01527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two-component regulatory system, response regulator protein rstA [imported] - Yersini C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AE0281
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, M.R.; Parkhill, 
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AE0281
                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-443 <HUN>
A;Cross-references: GB:M74177; NID:g169768; PIDN:AAA33894.1; PID:g169769
C;Comment: Rice alpha-amylaseses are encoded by three multigene families,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
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C;Superfamily: ompR protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AE0281
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: RAmy2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
JQ1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
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                                                                                                                             Matches
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Best Local
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Best Local
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Best Local
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   146 CRDDTQFSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DDRPYAD 9
||||||
13 DDRPYAD 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27/3; 71/1; 345/3
                                                              1 CRDDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRDDRPYADG
                                                                                                                         Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRDLRPHYDG
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Score 41; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                              10
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   155
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                                                                                                                                                   65.6%;
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                                                                                                                         Score 40; DB 2;
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
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red. No. 23;
Mismatches
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                                                                                                                                                                                     Length 443
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GSPDB:GN00175

0; Gaps

0,

밁 Q

C; Genetics:

0;

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Amy1, Amy2

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
S19990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amylase (EC 3.2.1.1) - rice
C;Species: Oryza sativa (rice)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S19990
R;Goldman, S.; Mawal, Y.; Wu, R.
hypothetical protein CC0876 [imported] - Caulobacter crescentus
c;Species: Caulobacter crescentus
c;Species: Caulobacter crescentus
c;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001" #text_change 20-Apr-2001
C;Accession: A87358
c;Naterman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
                                                                                                                                                                     RESULT 17
A87358
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: Rv3369
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv3369 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: H70971
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C; Superfamily: wheat alpha-amylase; alpha-amylase core homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 168-317/Domain: alpha-amylase core homology <AMY>
F; 202, 228, 314/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X64619; NID:g20172; PIDN:CAA45903.1; PID:g20173 C;Function:
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                                                                                                                                                                                                                                                                                                          ΩY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-445 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S19990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                    Best Lo
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,228,314/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                          101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-144 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.6%;
Similarity 60.0%;
6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S19990
                                                                                                                                                                                                                                                                                                                                                                 Similarity 6; Conserv
                                                                                                                                                                                                                                                                          CRDDAPY 107
                                                                                                                                                                                                                                                                                                CRDDRPY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRDDTQFSDG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                        Score 39;
Pred. No.
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2; Mismatches
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A, Cross references: GB:AE008688; PIDN:AAL42104.1;
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Gene: rpsf
A; Map position: circular chromosome
C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: AB2711
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                         A; Molecule type: DNA
A; Residues: 1-373 <EFS>
A;Cross-references: DDBJ:D10082; NID:g221456; PIDN:BAA00977.1; PID:g221458
                                                                                                                                                                                                                                                       C;Species: human herpesvirus 6
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: JQ1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AB2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S ribosomal protein S6 (imported) - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 *sequence_revision 11-Jan-2002 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005673; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87358
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A; Residues: 1-370 <STO>
                                                      A; Experimental source: strain Ull02 C; Superfamily: human herpesvirus 6
                                                                                                                                                         A; Reference number: A; Accession: JQ1648
                                                                                                                                                                                                                                                                                                                   SHL2 protein - human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-153 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Authors: Yoo, H.; Tao,
                                                                                                                                                                            A;Title: Identification of homologues to the human cytomegalovirus A;Reference number: JQ1647; MUID:92333249; PMID:1321206
                                                                                                                                                                                                                    R;Efstathiou, S.; Lawrence, G.L.; Brown, C.M.; Barrell, B.G
J. Gen. Virol. 73, 1661-1671, 1992
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                                                        human herpesvirus 6 SHL2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%;
77.8%;
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77.8%;
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Pred.
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Score 38;
Pred. No.
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No.
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14;
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21;
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                Length 373,
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T.; Levy, R.; Li, M.; McCl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (strain C58,
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Local Similarity

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-386 <13E>
A;Cross-references: EMBL:AB021506; NID:g499597; PIDN:BAA78223.1;
A;Experimental source: strain HST; pop. variant B
C;Genetics:
A;Note: U3
C;Superfamily: human herpesvirus 6 SHL2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20

RESULT 20

RESULT 20

RYA3662

hypothetical protein U3 [imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6

R:Variety: strain HST

C:Species: human herpesvirus 6

R:Variety: strain HST

C:Species: human herpesvirus 6

R:Copate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T43962

R:Isegawa, Y: Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; IVICOL. 73, 8053-8063, 1999

A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A:Reference number: 22732; MUID:99413319; PMID:10482554

A:Recession: T43962

A:Recession: T43962
RESULT 22
$12625
alpha-amylase (EC 3.2.1.1) 3D - rice C;Species: Oryza sativa (rice)
C;Date: 04-Dec-192 #sequence_revision
C;Accession: $12625; $12776; $15054; JT
                                                                                                                                                                                                                                   A;Experimental source: strain Z29; variant B C;Genetics: A;Note: U3 C;Superfamily: human herpesvirus 6 SHL2 protein
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Best Local S
Matches 6
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Best Local S
Matches 6
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%;
                                                                                                                                                                           Score 38; DB 2;
Pred. No. 22;
1; Mismatches
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Pred. No. 22;
1; Mismatches
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   on 04-Dec-1992 #text_change
JT0945
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S71804
nerve growth factor beta chain precursor C;Species: Gallus gallus (chicken) C;Date: 05-Oct-1988 #sequence_revision 05
                                           RESULT
A26311
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A; Residues: 1-435 < HUA>
                                                                                                                                                               Matches
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                                                                                                       56 RDDKPWFDG
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                                                                                                                                 2 RDDRPYADG 10
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6; Conser
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Nature 382, 547-551, 1996
A.Title: smoothened encodes a receptor-like serpentine protein requirely. Reference number: $71804; MUID:96320560; PMID:8700230
A. Accession: $71804
A. Molecule type: mRNA
A. Residues: 1-1024 <VAN>
A. Residues: intron-exon boundaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-emylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;170-314/Domain: alpha-amylase core homology CAMY> F;203,228,311/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor-like serpentine protein smoothened - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998 C;Accession: S71804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-72, /r', 75-136, 'R', 138-435 <ON2>
A; Cross-references: EMBL:M24287; NID:g169754; PIDN:AAA33886.1;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-435 CONES
A;Cross-references: EMBL:M24287
A;Cross-references: EMBL:M24287
A;Cross-references: EMBL:M24287
A;Cross-references: EMBL:M24287
A;O'Neil, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodri submitted to the EMBL Data Library, April 1989
A;Description: The alpha-amylase genes in Oryza sativa: Characterization of A;Reference number: S15054
A;Recession: S15054
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Nucleic Acids Res. 18, 7007-7014, 1990
A;Title: Structural organization and differential expression of rice alpha-amylase
A;Reference number: JT0945; MUID:91088278; PMID:2263460
A;Accession: S12625
                                                                                                                                                                                                                                                                                                                      62.3%;
66.7%;
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Pred. No. 58;
2; Mismatches
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Pred. No. 25;
1; Mismatches
   05-Oct-1988
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                                                     chicken (fragment)
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#text_change 21-Jul-2000
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RTERPYGDG

132

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 118-243 <WID>
A; Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:g222840; PIDN:BAA00008.1; PID
A; Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:g222840; PIDN:BAA00008.1; PID
A; Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:g222840; PIDN:BAA00008.1; PID
A; Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
A; Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
A; Reference number: A26312; MUID:86300647; PMID:2427334
A; Accession: S00127
A; Status: preliminary; not compared with conceptual translation
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A; Molecule type: DNA
A; Residues: 121-243 <MET>
A; Residues: 121-243 <MET>
A; Cross-references: GB: M26810; NID: g212446; PIDN: AAA48984.1;
A; Cross-references: Hallboeoek, F.; Ebendal, T.; Persson, H.
                                                                                                                                                    A;Cross-references: GB:M64783; NID:g153172; PIDN:AAA79278.1; PID:g153174 A;Note: sequence extracted from NCBI backbone (NCBIN:41300, NCBIP:41305) C;Superfamily: oleoyl-facyl-carrier-protein] hydrolase; oleoyl-facyl-carrier-F;16-228/Domain: oleoyl-facyl-carrier-protein] hydrolase homology <ACPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orf1 3'of bah - Streptomyces hygroscopicus
C:Species: Streptomyces hygroscopicus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A; Residues: 1-243 <EBE>
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R;Ebendal, T.; Larhammar, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;126-243/Product: nerve growth
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A; Residues: 126-243 <IBA>
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Best Local
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Pred. No.
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Pred. No.
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Brachet, P.;
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     R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                                       C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision
C;Accession: F87317
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RESULT 28
F87317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CPRD14 -
C;Species: Vigna unguiculata (cowpea)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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T11610
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A; Introns: 18/3; 167/3; 266/3; 36
C; Superfamily: human erythrocyte
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R;Blanchard, M.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
submitted to the EMBL Data Library, July 1996
submitted to the EMBL Data Library, July 1996
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submitted to the EMBL Data Library, July 1996
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                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-463 <BLA>
A;Cross-references: EMBL:U64847; PIDN:AAB04874.1; GSPDB:GN00023; CESP:F08F3.
A;Experimental source: strain Bristol N2; clone F08F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
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A; Residues: 1-325 < IUC>
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R; Blanchard, M.;
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hypothetical protein CC0551 [imported] - Caulobacter crescentus

20-Apr-2001 #text_change 20-Apr-2001

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trnA (guanine-N1-)-methyltransferase (EC 2.1.1.31) [imported] - Buchnera sp. (strain APS C;Species: Buchnera sp. (strain APS C;Species: Buchnera sp. (strain APS C;Species: D2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: C84976
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Tshikawa, H.
Nature 407, B1-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Accession: C84976
A;Accession: C84976
A;Accession: C84976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: trmD; BU396
C;Superfamily: tRNA (guanine-N1) methyltransferase
C;Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: F87317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <-STO>
A;Cross-references: GB:AE005673; NID:g13421742; PIDN:AAK22538.1; GSPDB:GN00148
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            propionyl-CoA carboxylase beta chain homolog - Saccharopolyspora erythraea C;Species: Saccharopolyspora erythraea C;Species: Saccharopolyspora erythraea C;Date: 10-Sep-1999 #text_change 16-Jun-2000 C;Date: 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: S71008 M.J.; Katz, L. R;Donadio, S; Staver, M.J.; Katz, L. Mol. Microbiol. 19, 977-984, 1996 Mol. Microbiol. 19, 977-984, 1996 A;Tete: Erythromycin production in Saccharopolyspora erythraea does not require a funct A;Tete: Erythromycin production in Saccharopolyspora erythraea does not require a funct A;Teterence number: S71005; MUID:96249691; PMID:8830278
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C84976
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C;Superfamily: propionyl-CoA carboxylase beta chain
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Query Match 59.0%;
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      Score 36; DB 2; Pred. No. 33; 0; Mismatches
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Run 8

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2 drosophila
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8 accharopol
3 homo saplen
6 buchnera apl
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13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Alpha-amylase type B isozyme precursor (EC 3.2.1.)
Blucan glucanohydrolase) (Clone PHV19) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORVU
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an activities of the statement is not removed.
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                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                  InterPro; IPR006589; Alp_amyl_cat_sub
InterPro; IPR006047; Alpha_amyl_cat.
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                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                 Calcium;
                                                                                                                                                                                                               Hydrolase; Glycosidase;
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Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                   BARLEY.
MISCELLANEOUS: TYPE B ISOZYME MRNA
CELLS AND INCREASES A HUNDRED-FOLD
GIBBERELLIC ACID.
SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dler P.M., Zwar J.A., Jacobsen J.V., Higgins T.J.V., Inglis A.S. effects of gibberellic acid and abscisic acid on alpha-amylase levels in barley aleurone layers studies using an alpha amylase
148
                                                                                                                                                                                                                                      PF00128; alpha-amylase; 1.
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P04063; 1AVA.
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 CRDDRPYADG
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                                                  Conservative
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                                                                                                                    >368
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 157
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                                                                100.0%;
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                Score 61;
Pred. No.
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                                                    Mismatches
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r (EC 3.2.1.1) (1,4-alpha-D-
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RESULT 2 AMY2_HORVU

PDB; PDB; PDB;

16-MAR-99. 15-JUN-99.

1AMY;

13-MAY-95.

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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. Menuet;
STRAIN-CV. Menuet;
MEDLINE-98298441; PubMed-9634702;
MEDLINE-98298441; PubMed-9634702;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase).
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P04063;
                                      EMBL;
EMBL;
PIR; P
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                           "Barley alpha-amylase bound to its endogenous protein inhibitorystal structure of the complex at 1.9-A resolution."; Structure 6:649-659(1998).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-94254083; PubMed-#196040;
Kadziola A., Abe J.-I., Svensson B., Haser
"Crystal and molecular structure of barley
J. Mol. Biol. 239:104-121(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Rahmatullah R.J., Huang J.K.,
Chandra G.R., Muthukrishnan S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide and predicted amino acid suffor high-pI alpha-amylases from barley plant Mol. Biol. 12:119-121(1989).
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Biol. Chem.
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INDUCTION: TYPE B ISOZYME MRNA IS U
CELLS AND INCREASES A HUNDRED-FOLD
GIBBERELLIC ACID.
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                                    ; X15226; CAA33298
; K02637; AAA98790
A31960; ALBHB.
                                                                                                an
                                                                                                             requires a license agreement
                                                                                                email to license@isb-sib.ch).
                                                                                                                                                                                                               THE ALPHA-AMYLASE FAMILY.
                                                     CAA33298.1;
AAA98790.1;
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alpha-amylase.";
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PRINTS; PRO0110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Hydrolase; Glycosidase; Carboh
Calcium; Multigene family; Sig
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha_amylase; 1.
      Carbohydrate metabolism; Seed; Germination; ly; Signal; 3D-structure.
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| REF: 2).
| 1).
     Ωy
                                         RT aleurones.";

RI J. Mol. Appl. Genet. 2:579-588(1984).

CC -1 CAPALYTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic CC -1 CAPALYTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic CC -1 CAPALYTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic CC -1 CAPALYTIC ACTIVITY: CC -1 Linkages in oligosaccharides and polysaccharides ACTIVITY.

CC -1 COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

CC -1 DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE ALPHA-AMYLASE. THE ENZYME THEN LOUGHER HITHIN 10 HOURS SITMULATES THE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE CC DEVELOPING PLANT EMBRYO.

CC -1 MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.

CC -1 MISCELLIANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CC GELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH CC GIBBERELLIC ACID.

CC SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (CLONE GRAWY56).
Rahmatullah R.J., Huang J.-K., Clark K.L., Reeck G.R.,
Rahmatullah R.J., Huang J.-K., Clark K.L., Reeck G.R.,
Chandra G.R., Muthukrishnan S.;
"Nucleotide and predicted amino acid sequences of two different genes
for high-pi alpha-smylases from barley.";
plant Mol. Biol. 12:119-121(1989).
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
MEDLINE-85159405; PubMed-6335720;
Huang J.-K., Swegle M., Dandekar A.M., Muthu
"Expression and regulation of alpha-amylase aleurones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
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     SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and
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Pred. No. 0.0009
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ylase gene family
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Calcium; M
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EMBL; K02636; AAA32932.1;
PIR; JE0406; JE0406.
HSSP; P04063; 1AVA.
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P17859;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Alpha-amylase precursor (EC 3.2.1.1) (1,4-a
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InterPro; IPR006047; Alpha_amyl_cat.
                                                                                                                                                                                                                                                                                                                                                Takeuchi H., Yamauchi D., Wada S.,
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A MEDLINE-94120017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamauchi
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SIGNAL
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15-JUL-1999 (Rel. 38, Last annotation update)
Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1
Alpha-amylase) (AMY1) (Low pI alpha-amylase)
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
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J. Biol. Chem.
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MEDLINE-83238423; Publ
Rogers J.C., Milliman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare (Barley). Stre Eukaryota; Viridiplantae; Stre Spermatophyta; Magnoliophyta; Triticae; Hordeum.
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SUBCELLUIAR LOCATION: EXTRACEILULAR.
DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZUME
THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
DEVELOPING PLANT EMBRYO.
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CAA51734.1;
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01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).

AMY1.1 OR AMY1A.

AMY1.1 OR AMY1A.
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ACT_SITE
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MEDLINE=9134657; PubMed=2102847;
Huang N., Sutliff T.D., Litts J.C., |
"Classification and characterization
                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota: Viridiplantae;
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O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
Rodriguez R.L.;
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PIR; A00846; ALBH.
HSSP; P04063; IAVA.
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
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318322; PubMed=2370848;
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n of the rice alpha-amylase
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01-JAN 1990 (Rel. 13, Created)
01-JAN 1990 (Rel. 13, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
28 Hypothetical protein RA0666.
29 RA1623;
N RA0666 OR SMA123;
S Rhizobium meliloti (Sinorhizobium meliloti).
30 Rhizobium SymA (megaplasmid 1).
31 Plasmid SymA (megaplasmid 1).
32 Plasmid SymA (megaplasmid 1).
33 Plasmid SymA (megaplasmid 1).
34 Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sinorhizobium/Ensifer group; Sin
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Kahn D.;
"fixK, a gene homologous with for and crp from Escherichia coli,
"egulates nitrogen fixation genes both positively and negatively
Rhizobium meliloti.";
EMBO J. 8:1279-1286(1989).
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MEDLINE=89305532; PubMed=2663474;
Batut J., Daveran-Mingot M.-L., David
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EMBL; M24286; AAA33885.1; ALT_INIT.
PIR; S10013; S10013.
HSSP; P04063; 1AVA.
Gramene; P17654; -.
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                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION.
MEDLINS-96017644; PubMed-7588066;
Hsu D.R., Chuang P.-T., Meyer B.J.;
"DPY-30, a nuclear protein essential early
Caenorhabditis elegans dosage compensation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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                                                                                                                              Chuang P.-T., Lieb J.D., Meyer B.J. "Sex-specific assembly of a dosage nematode X chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1994) to
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MEDLINE-95042743;
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                                                                    Science 274:1736-1739(1996).
                                                                                                                                                                                                                                                                                                                                Development 121:3323-3334(1995)
                                                                                                                                                                                                                                 MEDLINE=97094383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
FUNCTION: Involved in X dosage compensation chromosome. Required to reduce expression of both hermaphrodite X chromosomes. Its strong similarity with the condensin subunit smc4 suggests that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _CAEEL
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C646ED93410F1E09 CRC64;
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7 (Dumpty-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                Oryza sativa (Rice)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                      Alpha-amylase isozyme
                                                                                                                                                                                                                                                                                                                                                                                 P27935;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wormPep; R13G10.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T24216; T24216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                              STRAIN=cv. Japonica M202;
MEDLINE=92175526; PubMed=1541400;
Huang N., Reinl S.J., Rodriguez F
                                                                                                                                                                                                  Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza;
                                                                                                                                                                                                                                                                                                                 glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGEN
                       "RAmy2A; a novel alpha-amylase-encoding gene in rice.
Gene 111:223-228(1992).
                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                              AMY1.5 OR AMY2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AM2A_ORYSA
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: Consists of two putative central coiled-coil regions flanked by putative globular regions at the N- and C-termini. SIMILARITY: Belongs to the SMC family. SMC4 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified proteins.
SUBCELLULAR LOCATION: Nuclear. Associates with chromatin after 30-cell stage. It specifically localizes to the X chromosomes of wild-type XX embryos, but remains diffusely distributed throughout wild-type XX embryos, backware how 7K is required for its X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may reduce the X-chromosome transcript level chromatin structure during interphase cells. SUBUNIT: Component of a complex containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosome specific association.

DEVELOPMENTAL STAGE: Expressed in embryos and early-staged larvae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the nuclei of male (XO) embryos. Dpy-26 is required
    FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L35274; AAA62647.1; ... Z35602; CAA84669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF02483; SMC_C; PF02463; SMC_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DDRPYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long as its content and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDRPYAD 19
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356
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    IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Last annotation
2A precursor (EC
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                                                                                                                                                                                                                                                     Streptophyta;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
K->E,I: LOSS OF FUNCTION.
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Pred. No.
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COILED COIL (PC
                                                                                                                                                                                                                             Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled coil; Nuclear protein.
                                                                       R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF9043CA2AC23B06 CRC64;
                                                                                                                                                                                                                                                                                                                                          lon update)
(EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
15;
                                                                                                                                                                                                                                                       Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                Poaceae;
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RESULT 10
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Best Local S
Matches 6
SEQUENCE FROM N.A.

STRAIN-cv. Indica-IR26; TISSUE-Seed;

STRAIN-cv. Indica-IR26; TISSUE-Seed;

Goldman S., Mawal Y., Wu R.;

Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERN STARCH DURING GERMINATION.

-1- CATALTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

-1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

-1- SUBBURT: MODOMBEY.

-1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Alpha-amylase isozyme C2 precursor (EC 3.2.
glicanohydrolase).
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PP00128; alpha-amylase; 1.
lase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JQ1527; JQ1527.
P04063; 1AVA.
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precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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ALPHA - ANYLASE ISOZYME 2A.
ALPHA - ANYLASE ISOZYME 2A.
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CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
TBJF9264404F67F6 CRC64;
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Best Local S
Matches 6
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S6.
RPSF OR R01138 OR SMC00568.
Rhizoblum mellioti (Sinorhizoblum mellioti).
Racteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                   MEDLINE-21395507; PubMed-11481430;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S. Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Wedner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.; "Inco. Natl. Acad. Sci. U.S.A. 98:9879-9802(2001)."

-!- FUNCTION. Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS6_RHIME
Q92QZ7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X64619; CAA45903.1; -. PIR; S19990; S19990.
                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Pfam; PF00128; alpha-amylase; 1.
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                                                                                                                                                                                                                                                                       similarity)
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6; Conserv
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CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
DEDZ3701E836ACDA CRC64;
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Pred. No. 6.5;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Elanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizo
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD003809; Ribosomal_S6; 1.
TIGRFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL_S6; FALSE_NEG.
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      Science 294:2323-2328(2001).
-!- FUNCTION: Binds together with S18
                                                                                                                                                                                                                                                                                                                                                                                                 Cielo C., Slater S.; "Genome sequence of the plant pathogen and Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21608551;
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                                                                                                                                                                                                                                                                                                              similarity).
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149 AA; 17274 MW; 15766B6EEAE7F18C CR
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     AAL42104.1;
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TIGRFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL_S6; FALSE_NEG
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InterPro; IPR000529; Ribosomal_Ffam; PF01250; Ribosomal_S6; 1
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                                                                                                                                                                              EMBL; X83413; CAA58430.1;
EMBL; D10082; BAA00977.1;
PIR; JQ1648; JQ1648.
                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the succession of the statement of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession
                                                                                                                                                                                                                                                                                                                                                                                                                            and genome evolution.";
Virology 209:29-51(1995).
-i-SIMILARITY: BELONGS TO THE US22 FAMILY.
HUMAN CYTOMEGALOVIRUS UL24 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Efstathiou S., Lawrence G.L., Brown C "Identification of homologues to the family in human herpesvirus 6."; J. Gen. Virol. 73:1661-1671(1992).
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NCBI_TaxID=10370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=95266321; PubMed=7747482;
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MEDLINE=92333249; PubMed=1321206;
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                                                                                                                         SEQUENCE
                                                                                                                                          InterPro; IPR003360; Pfam; PF02393; US22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpesviridae;
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13;
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6: structure, coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones M., Thomson B.
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"clones and mrna expression during seed germination.";
"clones and mrna expression during seed germination.";
"clones and mrna expression during seed germination.";
"clones and mrna expression of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
"clones in oligosaccharides and polysaccharides."
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InterPro; IPR006047; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
Hydrolase; Glycosidase; Carbohydrate n
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; M24287; AAA33886.1; -.
PIR; S12625; S12625.
HSSP; P04063; 1AVA.
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Rodriguez R.L.;
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Nucleic
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Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
Alpha-amylase isozyme
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Acids Res. 18:7007-7014(1990).
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                                                                                                                                                                                                             ycosidase; Carbohydrate metabolism; Calcium;
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POTENTIAL.

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Liliopsida; Poales; Poaceae;
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HORMONE
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RESULT 15
SMO_DROME
RX MEDLINE-2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M. H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wel M. H., Ibeywam C.,
RA Liu X., Mattei B., McIntosh T.C., McCleod M.P., McPherson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
               QY
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Best Local
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p91682; Q9VPM8;
30-MAY-2000 (Rel. 39
30-MAY-2000 (Rel. 39
28-FEB-2003 (Rel. 41
Smoothened protein p
SMO OR CG11561.
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=96320560; PubMed=8700230; van den Heuvel M., Ingham P.W.; "smoothened encodes a receptor-like hedgehog signalling."; Nature 382:547-551(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein, a putative receptor Cell 86:221-232(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96319725; PubMed=870
Alcedo J., Ayzenzon M., von
"The Drosophila smoothened of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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39, Last sequence update)
41, Last annotation updat
n precursor (dSMO) (SMOH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8706127;
on M., von Ohlen T., No
moothened gene encodes
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encodes a seven-pass membrane
the hedgehog signal.";
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhau Y., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC OF EVERY SEGMENT POLARITY PROTEIN REQUIRED FOR CORRECT PATTERNING
CC OF EVERY SEGMENT G. PROTEIN-COUPLED RECEPTOR THAT ASSOCIATES WITH
CC THE DATCHED PROTEIN (PTC) TO TRANSDUCE THE HEDGEHOG (HH) SIGNAL
CC OF HEPORCHE PROTESIN (PTC) TO TRANSDUCE THE HEDGEHOG (HH) SIGNAL
CC OF HEPORCHE RECEPTOR THE ACTIVATION OF AN INHIBITORY G-PROTEIN. IN THE ABSENCE
CC OF HEPORCHE THE ACTIVATION OF AN INHIBITORY G-PROTEIN.
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EMBL; AF030334; AAB84775.1; -.

EMBL; AF030344; AAB84775.18.2; -.

FlyBase; FBgp0003444; smo.

GO; GO:0007350; P:blastoderm segmentation; IMP.

GO; GO:0007455; P:eye-antennal disc metamorphosis; IG:

GO; GO:000746; P:regulation of mitotic cell cycle; IN-

InterPro; IPR000039; Frizzled.

InterPro; IPR000034; Fz_domain.

InterPro; IPR000832; GPCR_secretin.
                     CARBOHYD
CARBOHYD
CARBOHYD
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PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00489; FRIZZLED. SMART; SM00063; FRI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send
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SUBCELLULAR LOCATION: Integral membrane
DEVELOPMENTAL STAGE: EXPRESSED AT ALL DE
THE LEVELS VARY.

SIMILARITY: BELONGS TO FAMILY FZ/SMO OF
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CAUTION: I
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                                                                                                 7 (POTENTIAL).
CYTOPLASMIC (POFE.
                                                                                                                                                                                 POTENTIAL.

SMOOTHENED PROTEIN.

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
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  POLY-SER.
N-LINKED
N-LINKED
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                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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AT ALL DEVELOPMENTAL
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                                                                                                                           (POTENTIAL)
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RESULT 16
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between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome polyprotein [Contains: N-terminal protein (P1); Helper component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa protein (C1); 6 kDa protein (C1); 6 kDa protein (C1); 6 kDa protein (C2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.1.48); Coat protein (CP)].

Lettuce mosaic virus (strain E) (LMV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97239892; PubM
Revers F., Yang S.J.,
Candresse T., Dunez J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparison of the complete nucleotide sequences of lettuce mosaic virus differing in their biological Virus Res. 47:167-177(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
-1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                      MAY BE INVOLVED IN REPLICATION.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CAPALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1' that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and
                                                                                                                       INDIVIDUAL PROTEINS.
SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                 terminus, commonly in the sequence "Tyr-Xaa-Val-Gly-|-Gly, processing of the potyviral polyprotein. PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA. PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                             {RNA}(N).
CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly
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CATALYTIC ACTIVITY:
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

in no way commercial

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RESULT 17

NGF_CHICK
ID NGF_C
AC P0520
DT 13-AU
DT 13-AU
DT 13-AU
DT 13-AU
DT 28-FE
DE Betra
GN NGFB.
OS Gallu
OC ELLKar
OC ELLKar
OC Archc
OC Galli
OX NCBI
RN (1)
RP SEQUI
RX MEDL:
RA ELBENT
RT "SLT;
RT gene
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Matches 6
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13-AUG-1987 (Rel. C
13-AUG-1987 (Rel. C
28-FEB-2003 (Rel. 4
Beta-nerve growth f
NGFB.
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Coat protein;
ATP-binding.
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                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-66300646; PubMed=3017695; Ebendahl T., Larhammar D., Persso "Structure and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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NP_BIND
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SEQUENCE OF 118-243 FROM N.A. MEDLINE-86248129; PubMed-3720959; Wion D., Perret C., Frechin N., K
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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m; PF00271; helicase_C; 1.

m; PF0085; Peptidase_C6; 1.

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m; PF00767; Pety_coat; 1.

m; PF00560; RNA_DEP_RNA_PO1; 1.

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915 CLDEAPYAD 29
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IPR001730;
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1410 1;
3255 AA;
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05, Last sequence update)
41, Last annotation update)
factor precursor (Beta-NGF).
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RNA_pol_P3D.
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NUCLEAR INCLUSION PROTE
NUCLEAR INCLUSION PROTE
NUCLEAR INCLUSION PROTEIN.
COAT PROTEIN.
ATP (POTENTIAL).
18 MW; B3E8582927E01628 CR
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Pred. No. 1.2e
1; Mismatches
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6 kDa PROTEIN 1.
CYTOPLASMIC INCLI
6 kDa PROTEIN 2.
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RESULT 18
PCCB_SACER
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EMBL; X04067; CAA27703.1; -.
EMBL; M26810; AAA48984.1; -.
PIR; A26311; A26311.
HSSP; P01139; 1BET.
InterPro; IPR002172; NGF.
PRINTS; P800268; NGF.
PRINTS; P800268; NGF.
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SEQUENCE
PCCB_SACER STANDARD; PRT; 5
P53003;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Propionyl-CoA carboxylase beta chain (
COA:carbon dioxide ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBRYONIC SENSORY NEURONS.

I SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.

SIMILARITY: BELONGS TO THE NGF-BETA, FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hallboeoek F., Ibanez C.F., Persson H.;;
"Evolutionary studies of the nerve growth facto
novel member abundantly expressed in Xenopus ov
Neuron 6:845-858(1991).

-i- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT
MAINTENANCE OF THE SYMPATHETIC AND SENSORY
STINULATES DIVISION AND DIFFERENTIATION OF
EMBRYONIC SENSORY NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 121-243 FROM N.A. MEDLINE-86300647; PubMed-242734; MEDLINE-86300647; PubMed-242734; Meler R., Becker-Andre M., Otz R., Heumann R., Shaw A., Thoenen i Meler R. Becker-Andre M. Gotz R., Heumann R., Shaw A., Thoenen i Melecular cloning of bovine and chick nerve growth factor (NGF): "Molecular cloning of bovine and chick nerve growth factor (NGF): Tellationship to the biological activity and antigenicity of NGF." (MGP) J. 5:1489-1493(1986).
                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
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"Molecular cloning of the avian transcription in brain.";
FEBS Lett. 203:82-86(1986).
[3]
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                                                                                                                                                         182
                                                                                                                                                                                                           Similarity
6; Conserv
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BY SIMILARITY.
BY SIMILARITY.
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(EC 6.4.1.3)
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IRX4_HUMAN

P78413; Q9UHR2;

15-JUL-1998 (Rel. 36, Created)

16-OCT-2001 (Rel. 40, Last sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of 
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   SEQUENCE OF Lewis M.T.,
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Bacteria; Actinobacteria; Actinobacteridae; Actinomyce
Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspo
                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=20092750; PubMed=10625552;

MEDLINE=20092750; PubMed=10625552;

Bruneau B.G., Bao Z.-Z., Tanaka M., Schott J.J.

Seidman J.G., Seidman C.E.;

"Cardlac expression of the ventricle-specific modulated by NKxZ-5 and dHand.";

Dev. Biol. 217:266-277(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia; I
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PRINTS; PR01070; ACCCTRFRASEB.
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InterPro; IPR000022; Carboxyl_trans.
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"Erythromycin production in Saccharopolyspora erythraea does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96249691; PubMed=8830278;
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Microbiol. 19:977-984 (1996).

CATALYTIC ACTIVITY: ATP+ propanoyl-CoA + HCO(3)(-) = ADP + Phosphate + (5)-methylmalonyl-CoA.

PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF ODD-CHAIN PATHWAY: ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.

SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX BIOTIN-CONTAINING ALPHA SUBUNITS & SIX BETA SUBUNITS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE ACCD / PCCB FAMILY.
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$71008; $71008.
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6; Conser
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; Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Primates; Catarrhini; Hominidae;
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   80-191 FROM N.A. Strickland P.A., family of human
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   Snyder C.J., I genes from the
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RESULT 20
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Best Local S
Matches 7
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P41778; 1DU6.
TRANSFAC; T04275; ...
Genew; HGNC:6129; IRX4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the endocellular bacterial symt
Buchnera sp. APS.";
Nature 407:81-86(2000).
-i- FUNCTION: Specifically methylates guanosine-37
                                                                                                                                   MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishiki
"Genome sequence of the endocellular bacterial symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRMD_BU
P57476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homeobox; DNA-binding; DNA_BIND 143 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1. SMART; SM00548; IRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox; 1. ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606199; -.
GO; GO:0007507; P:heart development;
                                                                                                                                                                                                                                                                           Enterobacteriaceae;
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                      Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                 methyltransferase) (tRNA [GM37]
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31)
                                                                                                                                                                                                           STRAIN=Tokyo
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                   symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                         TRMD OR BU396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR003893; Iroquois_homeo.
                     (By similarity).
CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
7; Conserv
                                                                                                                                                                                                        FROM N.A.
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519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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382 P
181 I
54444 MW;
  tRNA
                                                                                                                                                                                                                                                                                                     Buchnera.
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S-adenosyl-L-methionine + tRN/ containing N(1)-methylguanine.
                                                                                                                                                                                                                                                                                                                           Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36.5; D
Pred. No. 33;
2; Mismatches
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B2FFB278BEFC5AD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                        methyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
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                                                                                                                                                                                                                                                                                                                                Enterobacteriales;
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                                                                                                                                          Ishikawa
mbiont of
                          tRNA
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                                                                       various
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                          S-adenosyl-L-
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aphids
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RESULT 21
TRMD_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZW-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-methyltransferase) (tRNA [GM37] methyltransferase).
TRMD OR PM1297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AP001119; BAB1399.1; -
HANAP; MF_00605; -1
InterPro; IPR002649; tRNA_m1G_MT.
Pfam; PF01746; tRNA_m1G_MT; 1.
ProDom; PD004978; tRNA_m1G_MT; 1.
TIGRPAMS; TIGR00088; trmD; 1.
                                                    EMBL, AECOG168; AAKO3381.1; -.
HAMAP; MF_00605; -; 1.
InterPro; IPRO02649; ENNA_m1G_MT.
Pfam; PF01746; ERNA_m1G_MT; 1.
ProDom; PD004978; tRNA_m1G_MT; 1.
TIGREPAMS; TIGRO0088; trmD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).

1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + trna = S-adenosyl-L-homocysteine + trna containing N(1)-methylguanine.

1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-21145866; PubMed-11248100;
May B.J., Zhang Q., Li L.L., Paustlan M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales Pasteurellaceae; Pasteurella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella multocida
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Transferase; Methyltransferase; tRNA processing; Complete proteome
SEQUENCE 245 AA; 27494 MW; 6A35655295A59354 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 237; 18;
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TRMD_HAEIN
                                                                                                      Query Match
Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-9550630; PubMed-7542800;

MEDLINE-9550630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields D.M., Gotton M.D.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Seoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                        TIGR; H10202;

HAMAP; ME 00605; ; 1.

InterPro; IPR002649; tRNA_mIG_MT.

Pfam; PP01746; tRNA_mIG_MT; 1.

ProDom; PD004978; tRNA_mIG_MT; 1.

TIGREAMS; TIGR00088; trmD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.3)
methyltransferase) (tRNA [GM37] methyltransferase)
TRND OR HI0202.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U32705; AAC21871.1; -. PIR; C64054; C64054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurellaceae;
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gar
Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMD_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPALYTIC ACTIVITY: S-adenosyl-L-méthionine + tRNA = S-adenos homocysteine + tRNA containing N(1)-methylguanine. SUBCELLULAR LOCATION: Cytoplasmic (Potential). SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
CATALYTIC ACTIVITY:
homocysteine + tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ence 269:496-512(1995).
FUNCTION: Specifically methylates guanosine-37
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 DDRPYGGG
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                                                                                                      Similarity 6; Conserv
                                              DDRPYADG
                                                                                                                                                                                                                e; Methyltransferase;
246 AA; 27542 MW; |
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
   57
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                                                                                                                               59.0%;
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75
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                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                  Score 36; DB 1;
Pred. No. 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                ; tRNA processing; Complete
DEEF238159B1003D CRC64;
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .31) (M1G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 23
TRMD_YERPE
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                                                                Query Match
Best Local S
Matches 6
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EMBL; AE013692; AAM84480.1; ALT_INI
PIR; AIG399; AIG399;
HAMAP; MF_00605; -; 1
InterPro; IPR002649; tRNA_mlG_MT; 1.
Pfam; PF01746; tRNA_mlG_MT; 1.
ProDom; PD004978; tRNA_mlG_MT; 1.
                                                                                                                                                                                                                                                                                                                                                                                              between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBZBŪ9; Q8CWH8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31)
methyltransferase) (tRNA [GM37] methyltransferase).
TRMD OR YPO33293 OR Y0896.
                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-I- FUNCTION: Specifically methylates guan
                                                                                                                                   Transferase;
SEQUENCE 2
                                                                                                                                                                     TIGRFAMs; TIGRO0088; trmD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straley S.C., Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KIM5 / Biovar Mediaevalis; MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRMD_YERPE
                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encopean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                            homocysteine + tRNA containing N(1)-methylguanine.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA
50
                                                                Similarity 75.06; Conservative
DDRPYGGG
                                DDRPYADG
                                                                                                                                 Hethyltransferase; tRNA processing; Complete 246 AA; 27618 MW; DB800072F976ABCE CRC64;
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                                10
57
                                                                                59.0%;
75.0%;
                                                              Score 36; DB Pred. No. 19; 0; Mismatches
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                                                                              DB
19;
                                                                                                1;
                                                                 2;
                                                                                              Length 246;
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                                                                                                                                                                                                                                                                                                                                                                                           no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                 proteome
                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
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                                                                 Gaps
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RESULT 24
TRMD_VIBVU
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TRMD_BUCBP
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Best Local s
Matches 6
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31
methyltransferase) (tRNA [GM37] methyltransferase).
TRMD OR VV11617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                            15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last septence update)
15-SEP-2003 (Rel. 42, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence
submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8CWK5;
15-SEP-2003
                                                                      Buchnera aphidicola (subsp. Baizongia pistaciae)
Bacteria; Proteobacteria; Gammaproteobacteria; E
                                                                                                    TRMD OR BBP359
                                                                                                           methyltransferase) (tRNA [GM37]
                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Methyltransferase; SEQUENCE 249 AA; 28157 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016802; AA010036.1; -.
HAMAP; MF_00605; -; 1.
InterPro; IPR002649; tRNA_mIG_N
Pfam; PF01746; tRNA_mIG_MT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhee J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CMCP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio vulnificus.
SEQUENCE FROM N.A. MEDLINE=22426901;
                                                                                                                                                                         P59518;
15-SEP-2003
                                                                                                                                                                                                       TRMD_BUCBP
                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00088; trmD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRMD_VIBVU
                                           NCBI_TaxID=135842;
                                                          Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Specifically methylates guanosine-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homocysteine + trna containing N(1)-methylguanine.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA =
                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                      F01746; tRNA_m1G_MT; 1. PD004978; tRNA_m1G_MT; 1.
                                                                                                                                                                                                                                                                                                                                     similarity
6; Conserv
                                                                                                                                                                                                                                                                                                        DDRPYADG
                                                                                                                                                                                                                                                                            DDRPYGGG
                                                                                                                                                                                                                                                                                                                                   59.0%;
nilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim S.Y., Chung
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                                                                                                                                                                                                       STANDARD;
  PubMed=12522265;
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                                                                                                                                                                                                                                                                                                       10
                                                          Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tRNA_m1G_MT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ce of Vibrio vulnificus CMCP6.";
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                     0:
                                                                                                                                                                                                                                                                                                                                     Score 36; DB:
Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              ; tRNA processing; Complete proteome
BlCF66FBCE5D3A51 CRC64;
                                                                                                                 methyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrionales;
                                                                         Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jeong
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                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
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Gregor J., pa...
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Mau B., Shao Y.;
"The complete genome sequence of
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                                                                                                                                                                                                                                   MEDLINE-84067772; PubMed-6357787;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli, Escherichia coli 06, Escherichia coli 0157:H7, and Escherichia coli 0157:H7, and Shigella flexneri. Shigella flexneri. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia. ROBI_TaxID=562, 217992, 83334, 623;
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01-APR-1988 (Rel. 07, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (Migmethyltransferase).
methyltransferase) (tRNA (GM37) methyltransferase).
TRMD OR B2607 OR C3128 OR Z3901 OR ECS3470 OR SF2667.
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MEDLINE-2272406; PubMed-12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang
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Cheng H., Yao Z., He B., Chen R., Ma D;, Qiang B., Wen
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yobo T. Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-112106551;
Meria N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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EMBL; AE000346; AAC75656.1; -.
EMBL; D90888; BAA16492.1; -.
EMBL; D90888; BAA16492.1; -.
EMBL; AE015764; AAN81578.1; -.
EMBL; AE0015769; AAG57718.1; -.
EMBL; AE001529; ABB36893.1; -.
EMBL; AE0015282; BAB36893.1; -.
EMBL; AE0015282; AAN44162.1; -.
PIR; A30380; XXECG1.
PIR; B85907; B85907.
PIR; F91062; F91062.
ECOGene; EG11023; trmD.
PIR; F91062; F91062; -; 1.
InterPro; IPR002649; trNA_m1G_MT; 1.
ProDom; PD004978; tRNA_m1G_MT; 1.
ProDom; PD004978; tRNA_m1G_MT; 1.
TIGRPAMS; TIGR00088; trmD; 1.
TIGRPAMS; TIGR00088; trmD; 1.
TIGRPAMS; TIGR00088; trmD; 1.
TIGRPAMS; TIGR00088; trmD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.31)
methyltransferase) (tRNA [GM37] methyltransferase).
TRND OR STY2861 OR T2629.
                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamiln N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quali M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8Z4I5;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALTI
STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. I
                                                                                                                                                    Nature
[2]
                                                                                                                                                                                                                              enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                      "Complete genome sequence of a multiple enterica serovar Typhi CT18.";
                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THIS ENZYME IS PRESENT AT CA. 80 MOLECULES/GE SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY
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Pred. No.
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       Mayhew
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       G.F.,
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       Ď.J.
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Sebaihia M.,
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Best Local
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                                                                                                                                                                                                                  STRAIN=LT2;
Persson B.C.
Submitted (SI
                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31)
methyltransferase) (tRNA [GM37] methyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. -! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                        McClelland M., Sanderson K.E., Spieth J., Cl. Courtney L., Porwollik S., Ali J., Dante M., Leonard S., Nguyen C., Scott K., Holmes A., (Syan E., Sun H., Florea L., Miller W., Stone) Waterston R., Wilson R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL627276; CAD05853.1; -.
EMBL; AC016843; AA070200.1; -.
EMBL; D0605; -1.
InterPro; IPR002649; tRNA_mlg_MT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                          Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Methyltransferase; tRNA processing; Complete SEQUENCE 255 AA; 28318 MW; B96812A32091495F CRC64;
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ProDom; PD004978; tRNA_m1G_MT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burland V.,
                                                                                                                                                             STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burland V., Kodoyianni V., Schwartz D.C., Blattner F
"Comparative genomics of Salmonella enterica serovar
           -!- FUNCTION: Special (By similarity)
-!- CATALYTIC ACTIV
                                                                                                                                                                                                                                                                                  NCBI_TaxID=602;
                                                     Nature 413:852-856(2001)
                                                                              "Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD
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CATALYTIC ACTIVITY:
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homocysteine
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6; Conser
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                                                                              genome
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S-adenosyl-L-methionine + tRNA containing N(1)-methylguanine.
                                                                               of
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There are no restrictions
ng as its content is in
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                                                                               enterica
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                                                                                                                       Clifton S.W., Latreille P.,
M., Du F., Hou S., Layman D.
., Grewal N., Mulvaney E.,
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RESULT
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EMBL; AE008821; ALIZ1563.1; -.
PIR; S37175; S37175.
STyGene; SG10395; trmD.
HAMAP; ME_00005; ; 1.
InterPro; IPR002649; trNA_mIG_MT.
Pfam; PF01746; tRNA_mIG_MT; 1.
PrODOm; PD004978; tRNA_mIG_MT; 1.
TIGREAMS; TIRR0088; trNA_mIG_MT; 1.
TIGREAMS; TIRR0088; trNA_mIG_MT; 1.
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_SERMA
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-SM6;
MEDLINE-94320777; PubMed-8045416;
Jin S., Benedik M.J.;
"Sequences of the Seyratia marcescens rplS and trmD genes.";
Gene 145:147-148(1994).
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                   EMBL; L23334; AAA50783.1; -
HAMAP; ME_00605; -; 1
InterPro; IPR002649; tRNA_m1G_MT.
Pfam; PF01746; tRNA_m1G_MT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.3
methyltransferase) (tRNA [GM37] methyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serratia marcescens.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRMD_SERMA
P36244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Serratia.
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255 AA; 28348 MW; A9691ED23CE1495F CRC64;
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75.0%;
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Pred. No.
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TRMD_BUCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
methyltransferase) (tRNA [GM37] methyltransferase).
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Transferase; Methyltransferase; tRNA processing.
SEQUENCE 255 AA; 28465 MM; 48A71576D9B3A50B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-22084549; PubMed-12089438;
Tamas I., Klasson L., Canbaeck B.,
Tamas I., J., Sandstroem J.P., t
Wernegreen J.J., Sandstroem J.P., t
"50 million years of genomic stasts"
                                                                                                                                                                                                                                                                                       InterPro; IPR002649; tRNA_mIG_MT.
Pfam; PF01746; tRNA_mIG_MT; 1.
ProDom; PD004978; tRNA_mIG_MT; 1.
TIGREAMS; TIGR00088; trmD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE014114; AAM67935.1;
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Bacteria; Proteobacteria; Gammaproteobacteria; E
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Specifically methylates guanosine-37 in various trnas (By similarity).

(ATRIVIC ACTIVITY: S-adenosyl-L-methionine + trna - S-adenosyl-L-homocysteine + trna containing N(1)-methylguanine.

SUBCELIULAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
3 DDRPYADG 10
||||| |
67 DDRPYGGG 74
   67
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                                                                                                               6; Conserv
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Similarity 75.0%;
6; Conservative
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                                                                                                               Conservative
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52 AA; 30500 MW; 653A65B1663A04CA CRC64;
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75.0%;
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                                                                                                                  2;
                                                                                                                                                                        Length 262;
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     protein search, using sw model
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2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_manmal:*
8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_acteri
17: sp_archeaf
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Alpha-amylase precursor (1:
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InterPro; IPRO06046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PRO0110; ALPHAAMYLASE.
SEQUENCE 427 AA; 47402 MM; D21BA
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldea
Triticeae; Hordeum.
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Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.

"Structure and organization of two divergent alpha-amylase barley.";
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                                                                             Spermatophyta; Magnoliophyta; Triticeae; Hordeum. NCBI_TaxID=4513;
                                                                                                                                                                      Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
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SEQUENCE FROM N.A.
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Q8xv03 ralstonia s
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1 01-MAR-2003 (TrEMBLrel. 23, Last annotation u
1 Barley (H.vulgare) alpha-amylase 1.
1 Barley (H.vulgare) Barley).
2 Eukaryota; Viridiplantae; Streptophyta; Embrication vulgare (Barley).
3 Eukaryota; Viridiplantae; Streptophyta; Embrication vulgare (Barley).
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006546; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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J. Biol. Chem. 263:18953-18960(1988).
EMBL; J04202; AAA98615.1;
HSSP; P04063; LAVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. muthukrishnan S.; Submitted (JUL-1988) to the EMBL/GenBank/DDBJ databases. EMBL; M17125; AAA32926:1; -. HSSP; P04063; 1AVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and organization coarley.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol.
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                                                                                                                                                                                                                                         Similarity 9; Conserv
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427 ×
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  (TrEMBLrel. 01,
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                                               PRELIMINARY;
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a-amylase 1.
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    Created)
                                                                                                                                                                                                                                         Score 56; DB Pred. No. 0.04 0; Mismatches
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ALPHA-AMYLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chandra
                                               PRT;
                                                                                                                                                                                                                                                                                                                                4E7B8B741C944095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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divergent alpha-amylas
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ches 0;
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Matches
                                                                                                      SEQUENCE FROM N.A.

Matthews P.R., Gubler F., Jacobsen J.V.;
Ma plant-based expression system for match
1802ymes.";
Submitted (FEB-1997) to the EMBL/GenBank/DJ
EMBL; Y11277; CAA72144.1;
EMBL; Y11277; CAA72144.1;
InterPro; IPR00639; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Defen: p804184.
                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   004965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             whittier R.F., Dean D.A., Ro
Submitted (FEB-1991) to the
EMBL; X05166; CAA-8803.1; -.
EMBL; M15208; AAA32935.1; -.
HISSP, P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogers J.C., Milliman C.;
"Coordinate increase in major transcripts from the high pI alpha-amylase multigene family in barley aleurone cells stimulated with gibberellic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Whittier R.F., Dean D.A., Rogers J.C.; Nucleic Acids Res. 13:0-0(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMTI OR AMT32B."
HOrdeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2003 (TrEMBLrel. 23, Alpha-amylase (EC 3.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO06047; Alpha_amyl_cat.
InterPro; IPRO06589; Alp_amyl_cat.sub.
InterPro; IPRO06046; Glyco_hydro_13.
Pfam; PF00128; alpha_amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Whittier R.F., Dea
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01-MAR-2003 (TrEMBLrel.
                                                           SMART;
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                   rero; IPRO06589; Alpha_amyl_cat.
PF00128; alpha-amylase; 1.
; SM00642; Aamy; 1.
sldase; Hvdrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 CRDDTKYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRDDRPYADG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; PR00110; ALPHAAMYLASE.
SM00642; Aamy; 1.
CE 421 AA; 46102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 80.88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem.
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   47770 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogers J.C.;
he EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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   67E910E7CB7769E4 CRC64;
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Q8GURO;
01-MAR-2003 (TTEMBLTel. 2
01-MAR-2003 (TTEMBLTEL 2
01-MAR-2003 (TTEMBLTEL 2
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Q8LJQ6;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Nanicac; TISSUE-Fruit;
Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
Sequencing and molecular characterization of a banana alpha-amylase
CDNA clone related to the fruit ripening";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF533646; AAN01149.1;
InterPro; IFR0066047; Alpha_amyl_cat.
InterPro; IFR006699; Alp.amyl_cat.
InterPro; IFR006699; Alp.amyl_cat.
InterPro; IFR006699; Alp.amyl_cat.
InterPro; IFR006046; Glyco_hydro_13.
Ffam; PF00128; alpha-amylase; 1.
FRINTS; FR00110; ALPHAAMYLASE.
ENART; SM00642; Aamy; 1.
                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotatic
Alpha-amylase precursor (EC 3.2.1.1).
Musa acuminata (Banana).
Eukaryota, Viridiplantae, Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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Musa acuminata (Banana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
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SIGNAL 1 15 P
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"Sequence and molecular characterization of the alpha-amylase expressed during maturation of the banana (Musa spp.).";
Thesis (2001), Universidade de Sao Paulo, Sao Paulo, Brasil.
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SEQUENCE FROM N.A.
                                                              NCBI_TaxID=4641;
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416 AA;
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80.0%;
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a; Zingiberales; Musaceae;
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Matches 7
        Q40018 PRELIMINARY; PRT; 437 AA.
Q40018;
Q40018;
C1-NOV-1996 (TrEMBLrel. 01, Created)
P 01-NOV-1996 (TrEMBLrel. 02, Last sequence update)
P 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Barley (H.vulgare) alpha-amylase 2.
Hordeum vulgare (Barley).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
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O04964; OTEMBLE 04, C:
01-JUL-1997 (TREMBLE 04, L:
01-JUL-1997 (TREMBLE 04, L:
01-MAR-2003 (TREMBLE 23, L:
Alpha-amylase (EC 3.2.1.1).
AMY.
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ
EMBL; AY171068; AAO11776.1; -.
Signal; Hydrolase; Glycosidase.
Signal 1 15 POTENTIAL.
SIGNAL 1 15 POTENTIAL.
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1997) to the EMBL; Y11276; CAA72143.1; -. HSSP; P04063; IAVA.
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NCBI_TaxID=4513;
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Vieira A. Jr., Nascimento J.R.O., Lajolo F:M.;
"Sequencing and molecular characterization of
                                                                                                                                                                                                                                                                  SEQUENCE
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Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                 Local
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437 AA; 477
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yta; Liliopsida; Poales; Poaceae; Pooidea
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7D5ECE630F221915
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5.5;
                     Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooideae;
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006646; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
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01-MAR-2003 (TrEMBLrel.
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EMBL; M17127; AAA32928.1; -.
HSSP; P04063; 1AVA.
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"Structure and organization of two di
barley.";
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Knox C.A.P., Sonthayanon B.,
"Structure and organization
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta;
                    Eukaryota;
                                         Avena fatua.
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InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
SEQUENCE 438 AA; 47824 MW; 38945AF
Spermatophyta;
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M17128; AAA32927.1;
P04063; 1AVA.
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Viridiplantae; Stroyta; Magnoliophyta;
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EMBL, AJ010728; CAA09323.1; -.
HSSP; PA0403; 1AVA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alphamyl_cat_sub.
InterPro; IPR006589; Alphamyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase: 1.
PRINTS; PR00110; AlpHAMYLASE.
SMART; SM00442; Aamy; 1.
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                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDILINE-99077315; PubMed-9862499;

Willmott R.L., Rushton P.J., Hooley R., Lazarus C.M.;

Willmott R.L., Rushton P.J., Hooley R., Lazarus C.M.;

"DNasel footprints suggest the involvement of at least t
transcription factors in the regulation of alpha-Amy2/A
glaberellin ", as a second of a second plant Mol. Biol. 38:817-825(1998).

EMBL; AJO10729; CAA09324.1; -.

MISSP; P04063; LAVA.

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InterPro; IPR006589; Alp_amyl_cat.sub.
InterPro; IPR006046; Glyco.hydro_13.
Pfam; Pf00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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Avena fatua.

Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Aveneae; Avena

ACBI_TaxID-4499;
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Thesis (1994), University of Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Willmott R.L.;
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NCBI_TaxID=4499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tt R.L.;
(1994), University of Bristol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRDDRPYADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
7; Conservat
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
3.2.1.1).
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    POTENTIAL.
ALPHA-AMYLASE.
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Pred. No. 16;
l; Mismatches 2
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499F8C3E9767C1E1 CRC64;
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004272;
004272;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Chitinase (Fragment).
Cryza sativa (Rice).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
SEQUENCE FROM N.A.

MORIH., KOBAYASHIT., TONOKAWA T., Tatematsu A.,
KIMURA A., Chiba S.,
MOLecular Cloning of an alpha-Amylase cDNA from
cotyledons of kidney bean (Phaseolus vulgaris L.
J. Appl. Glycosci. 45:261-267(1997).
                                                                                                                                                                                                                                                                                                                                                                          09ZP43;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
Phaseolus vulgaris (Kidiney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Fabales; Fabaceae; Papillonoideae; Phaseolus.
NCBI_TaxID=3885;
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Pfam; PP00182; Glyco_hydro_19; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
NON_TER 1 1
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STRAIN=cV. IR36; TISSUE=Leaf;
Yun C.-H., Lee M.-C., Lee J.S., Yun K.J., Eun M.Y.;
"Isolation and characterization of a rice chitinase cDNP
rice blast fungus-infected rice leaves.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; aF001501; AAB58239.1; -.
HSSP: P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ZP43
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; Pred. No. 16;
1; Mismatches
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    Mismatches

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Pred. No.
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                                                                                                                                          Tatematsu A.,
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cv. Toramame).";
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; aggnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Convolvulaceae; Cuscuta.
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HSSP; P04063; 1AVA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and nucleotide sequence of detachment amylase from Cuscuta reflexa.";
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases
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Ramachandiran S., Srinivasa B.,
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      (Violet)
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9A3ECA606C7BB60A CRC64;
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Pred. No. 24;
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9EF67F8496C2A9F3 CRC64;
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alpha-Amylase in Developing Seeds of Mor
plant Physiol 129:1045-1053(2002).
EMBL; AB077387; BAC02435.1; .
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat.sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; Pf00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
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MEDLINE=22111127; Pubb
Nakayama A., Park S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
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Eukaryota; Metazoa; Arthropoda; Harapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                          Patel S., Phouanenavong Celniker S.;
                                                                                                                                                                                   EMBL; AY094789; AAM11142.1; -
FlyBase; FBgn0025726; unc-13.
                                                                                                                                                                                                                        Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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OR CG2999.
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REPAIRM-Berkeley;
RX MEDILINE-2019600; PubMed-10731132;
RX MEDILINE-2019600; PubMed-10731132;
RX MEDILINE-2019600; PubMed-10731132;
RX Adams M.D., Cellaiker S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Adams M.D., Cellaiker S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Adams M.D., Cellaiker S.E., Richards S., Ashburner M., Henderson S.N., Ra Adams M.D., Levis S.E., Richards S., Ashburner M., Henderson S.N., Ra Adams M.D., Cellaiker S.E., Richards S., Ashburner M., Henderson S.N., Ra Borton G.G., Wortman J.R., Kindell M.D., Zhang O., Chen L.W., Pacific R.B., Lowers M. Chardell M.D., Zhang O., Chen M.D., Rang B.D., Rang M. R.C., Busam D.A., Burtis R.C., Herard M.D., Zhang O., Chen J.D., Rang B.D., Rang M. R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Busam D.A., Burtis R.C., Burtis R.D., Boltchan M.R., Bonck J. Brokstein P., Burtis R.A., Bonck J., Wei M.-H., Ibegvam C., Ra Borton B.D., Boltchan A.E., Garg N.S., Gelbart W.M., Classer K.M., Royaland T.J., Hernandez J.R., Houck J.R., Ra Borton B.D., Boltchan A.E., Garg N.S., Gelbart W.M., Classer K.M., Royaland T.J., Hernandez J.R., Houck J.R., Ra Borton R.C., Ratic C.D., Kraft C., Kravitz S., Kulp D. Lai Z., Ra Hartis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.A., Ra Hartis N.L., Salash F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Hartis N.L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Hartis N.L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Hartis N.L., McIncosh T.C., McLood M.P., Neiher D.L., Nation J.A., McIncosh T.C., McLood M.P., Neiher D.L., Nation D.L., Nation N.A., Nixon K., Neiberen D.R., Neiberon D.L., Nation N.A., Nixon K., Nixon K., Neiberen D.R., Neiberon D.L., Nation J.A., Neiberon D.L., Nation J.M., Nixon M., Skipski M.P., Smith T.T., Ra Martis M.D., Neiberon D.L., Nation M.R., Neiberon D
   SEQUENCE FROM N.A.
Misra S., Crosby M.,
Hradecky P., Huang
Tupy J.L., Bergman (
Clamp M., Drysdale )
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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.S., Prochnik S.E., Smicarlson J.W., Celniker Frise E., de Grey A., )
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RP MEDLINE=20196006; pubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Harn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Harn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Harl J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan D.A., Butler H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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L SUBMILLED (SEEP-2002) to the EMBL/GenBank/DDBJ databas C -1 - SIMILLARITY: CONTAINS 2 C2 DOMAINS.

R HSSP; P28867; 1PR0.

R F1YBASE, FB900025726; unc-13.

R InterPro; IPR002008; C2.

R InterPro; IPR002219; DaG-PE-Dind.

R Ffam; PF00136; C2; 2.

R Ffam; PF00136; C2; 2.

R Ffam; PF00136; C2DOMAIN.

R PFANTS; PR00306; C2DOMAIN.

R PRINTS; PR00008; DAG-PE-DIND_DOM_1; 1.

R SWART; SM00109; C2; 1.

R SWART; SM00199; C2; DOMAIN_2; 1.

R PROSITE; PS00479; DAG-PE-BIND_DOM_1; 1.

R PROSITE; PS00479; DAG-PE-BIND_DOM_1; 1.

R PROSITE; PS00479; DAG-PE-BIND_DOM_1; 1.

R PROSITE; PS00479; DAG-PE-BIND_DOM_1; 1.

R PROSITE; PS00479; DAG-PE-BIND_DOM_1; 1.

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Adams M.D., Celniker
Submitted (MAR-2000)
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"Annotation of Drosophila melanogaster genome.";
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e EMBL/GenBank/DDBJ
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.R.,
RA McRiclov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHolov G., Mitshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhang J., Yao Q.A., Ye J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RI Science 287:2185-2195(2000).
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Q8ZE74
ID Q8ZE7
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Celniker S.E., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
A Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Moshrefi A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Holder J., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A Milliams J., Paragas V., Park S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Tsequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Pannotation of Drosophila melanogaster genome."
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ilarity 100.0%;
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    PRT;
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hes 0;
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RA Baker S., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RA Nature 413:523-527(2001).
R EMBL; AJ414151; CAC91113.1; -.
REMBL; AJ414151; CAC91113.1; -.
REMBL; AJ414151; CAC91113.1; -.
R Ffam; PF00072; response_reg; 1.
PFam; PF00072; response_reg; 1.
PFam; PF00072; response_reg; 1.
R ProDom; PD000039; Response_reg; 1.
R ProDom; PD000039; Trans_reg_C; 1.
R ProDom; PD000039; Trans_reg_C; 1.
R ProDom; PD000039; Trans_reg_C; 1.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                               SEQUENCE FROM N.A.

STRAIN-KIM5 / Biovar Mediaevalis;

MEDLINE-22137863; PubMed-12142430;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayh

Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.

Petherston J.D., Lindler L.E., Brubaker R.R., Plano G

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S

Perry R.D.;
                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Response transcriptional regulatory protein (RstB
RSTA OR Y2139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.
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RSTA OR YPO2308.
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Bacteria; Proteobacteria; Gar
Enterobacteriaceae; Yersinia
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Enterobacteriaceae; Yersir
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                                                                                   "Genome sequence of Yersinia
                                  Bacteriol, 184:4601-4611(2002).
BL; AE013817; AAM85701.1; -
QUENCE 266 AA; 30220 MW: FFK1/
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E; PS50110; RESPONSE_REGULATORY; 1.
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70.0%;
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Pred. No.
    Score 40;
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Matches 7
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X Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Batut J.,

A Capela D., Barloy-Hubler F., Gonzy J.,

Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Weidner S., Gallbert F.;

"Analysis of the chromosome sequence of the legume symbiont

"Analysis of the chromosome sequence of the legume symbiont

"Shorhizohum mellioti strain 1021.";

"Proc. Natl. Acad. Sci. U.S. A. 98:9877-9882(2001).

RE EMBL; AL591784; CAC45350.1.

RE PFEND: PRO2913; FAD-oxidase_C.

RINTERPO; IPR006094; Oxid.FAD_bind.

RR Pfenn; PF02515; FAD-binding_4; 1.
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Q92RS2;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-CCT-2002 (TrEMBLrel. 2, Last annotation update)
Probable 91ycolate oxidase subunit protein.
GLCE OR R00778 OR SMC00833.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rh.
Rhizobiaceae; Sinorhizobium.
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SEQUENCE FROM N.A.

STRAIN-A3(2) / M145;

MEDILINE-21996410; PubMed-12000953;

MEDLINE-21996410; MISSER H., Outlins M., Kieser H., Gobbe A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
                                                                                                                                                                                                                                                                       Q93JI3; PRELIMINARY;
Q93JI3;
Q1-DEC-2001 (TIEMBLITE1. 19,
Q1-DEC-2001 (TIEMBLITE1. 19,
Q1-MAR-2003 (TIEMBLITE1. 23,
                                                                                                                                                                                                          Partial putative replication
SC03995 OR SCBAC25E3.32.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Ac
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STRAIN-1021;
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Last sequence update)
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n initiator protein (Fra
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Pred. No.
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Matches
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Best I
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O50338;
O50338;
O50338;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3369.
Rv3369 OR MTW004.27 OR MT3478.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomyce
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
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                                                                                                                                                                                         "Whole genome comparison of Mycol laboratory Strains.";
Submitted (APR-2001) to the EMBL, EMBL; AL009198; CAA15754.1; -.
EMBL; AE009198; CAA15754.1; -.
EMBL; AE0091754; ANAK47816.1; -.
TIGR; MT3478; -.
TIGR; MT3478; -.
Tuberculist; Mr369; -.
Typothetical protein; Complete pi
SEQUENCE 144 AA; 15718 MW; 9;
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GCole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
GCole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F.,
Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hoiroyd
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Dodson R.G., Gwinn M.L., Haft D., Hickey E., Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Ncolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939118; CAC44719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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101
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                                                                                                 Conservative
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No. 17;
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RESULT 09A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID 97A9T6 ID
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Best Loc
Matches
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O987T8;
O1-ocr-2001 (TremBirel 18, Cr
O1-ocr-2001 (TremBirel 22, L
O1-ocr-2002 (TremBirel 22, L
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01-JUN-2001
01-JUN-2001
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MARF303099;
MEDIJINE-2108230; PubMed=11214968;
MEDIJINE-2108230; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Kimura T., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
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NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9A9T6
                                                                                                                                                                                                                                                                        Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                              Takeuchi C., Yamada M., Tabata
"Complete genome structure of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phyllobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete SEQUENCE 370 AA; 42422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21173698;
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                                                                         Pfam; PF02913; FAD-oxidase_C; Pfam; PF01565; FAD_binding_4;
                                                                                                                                                   EMBL; AP003010; BAB53112.1; -.
InterPro; IPR004113; FAD-oxidase_C
InterPro; IPR006094; Oxid_FAD_bind
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       proteome.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
protein CC0876.
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1D8908E0CBCDF357
       82C9A44BAD0B3475
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No. 48;
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                                                                                                                                                                                                                                                                                                                                         Matches
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"Analysis of vsp72-like sequences in submitted (FEB-2000) to the EMBL/Gen EMBL; AF236019; AAF69832.1; ...

InterPro; IPR006209; EGF-like.

InterPro; IPR005212; Furin_repeat.
InterPro; IPR005212; Giardia_VSP.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Variant-specific surface protein VSP MM/Sac-C/1 (Fragment).
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID-5741;
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PROSITE; PS01248; LAMININ_TYPE_
NON_TER 1
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Pfam; PF03302; VSP; 1
SMART; SM00181; EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00181; EGF; SMART; SM00261; FU;
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer
                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                 01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                    Q9Y113
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                                                                                                                                          Drosophila melanogaster (Fruit i
Eukaryota; Metazoa; Arthropoda;
                                                                                                       NCBI_TaxID=7227;
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RA Beleson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kadush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nuxskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Stanpson M., Skupski M.P., Smith T.,
RA Rainert K., Fertor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weissen S.M., Woodage T., Worley R.C., Wu D., Yang S., Yao Q.A.,
RA Weissen S.M., Shong W., Zhan M., Zhan S., Zhu X., Smith H.O.,
RA Jeng X.H., Zhong F.N., Zhong W., Zhong X., Zhu X., Smith H.O.,
Ra Jeng X., Yao Q.A., Zheng Y., Zhu X., Smith H.O.,
Ra Jeng X., Yao Q., Zheng 
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01-OCT-2002 (TrEM
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Variable surface)
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Abril J.F., Ao
Ballew R.M., I
Beeson K.Y., I
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"Full length Drosophila melanogaster cDNA sequence.";
"Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF046569; AND38634.1;
EMBL; AF146569; AND38634.1;
EMBL; AF146569; AND38634.1;
ENDSER FB900077553; BCDNA:GH10333.
InterPro; IPR001395; Aldo/Ket_Ted.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
SEQUENCE 594 AA; 67934 MW; D5A87283888A97F4 CRC64;
                       Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae;
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazel, G.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
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InterPro; IPRO06212; Furin_repeat.
InterPro; IPRO06212; Giardia_VSP.
InterPro; IPRO06127; Giardia_VSP.
Pfam; PF03302; VSP; 2.
SMARR; SM00261; FU; 5.
PROSITE; PS01186; EGF_2; 1.
SEQUENCE 739 AA; 76763 MW; 511A7
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Q9GS24;
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MORTANEZ C.;

MA 63kDa VSP9B10-like protein expressed in the C-8 Glardia duodenalis "A 63kDa VSP9B10-like protein expressed in the C-8 Glardia duodenalis Mexican clone.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ457171; CAD29801.2; -

InterPro; IPR006209; EGE_like.

InterPro; IPR005127; Giardia_VSP.

PFAm; PF03302; VSP; 1.

PROSTTE; PS01186; EGE_2; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
variant-specific surface protein VSP9B10.
61ardia lamblia (Giardia intestinalis).
Eukaryota: Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect.
EMBL; AY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21117019; PubMed=11179375;
Nash T.E., Lujan H.T., Mowatt M.R., Conrad (
"Variant-Specific Surface Protein Switching Infect. Immun 69:1922-1923(2001).
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STRAIN-PORTLAND 1 (P1);
Bermudez-Cruz R., Ortega-Pierres G., Ceja V., Coral-Vazquez R.,
Fonseca R., Cervantes L., Sanchez A., Depardon F., Newport G.,
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                                                                                                         1:||:||
244 CKDDKPY 250
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                                                                                                                                                            1 CRDDRPY 7
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witching in Giardia lamblia.";
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Title: Perfect score: Sequence:

US-09-830-876-3 56 1 VNWVNKVGGS 10

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                                                                                                                                                                                            Two site immunoassay for the qualitative or quantitative detection alpha-amylase in a test sample, used to detect weather damage in a cereal grain, such as wheat, rye, triticale or barley -
                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                      Skerritt JH;
                                                                                                                                                                                                                                                                                           (QUAL-) QUALITY WHEAT CRC LTD
                                                                                                                                                                                                                                                                                                                  11-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cereal grain
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                                                                                                            The present sequence represents a wheat alpha-amylase. Antibodies which recognise epitopes from this protein are used in a two-site immunoassay for qualitative or quantitative detection of alpha-amylase in a test sample. The assay is used for detecting weather damage in a cereal grain. Weather damage is caused by the action of hydrolytic enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate the breakdown of starch granules and protein in the endosperm of germinating grain. Individual growers can identify areas of sprouting prior to harvest, preventing contamination of sound wheat by weather damaged wheat. The damaged grain can be harvested separately from the sound grain and financial losses resulting from down grading the whole or silo (elevator) receival of grain or can be used on farms with minimal contamination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VNWVNKVGGS
 1 VNWVNKVGGS
                          10;
                                       Similarity
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                                                                             425
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                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               98AU-0007058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-AU00995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
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                                       100.0%;
                           0;
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                                       Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-site immunoassay; weather damage;
                            Mismatches
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0.0061;
                                                     DB 21;
                                        . 29;
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                            0,
                                                   Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                            Indels
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                            Gaps
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AAM50253
ID AAM50253 standard; F
XX
AC AAM50253;
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                                                      Query Match
Best Local S
Matches 8
                                                                                                                                The present sequence is that of alpha-amylase encoded by DNA clone alpha-Amy3-C (see AAI70540). Expression of alpha-Amy3-C increases to the use of an alpha-amylase gene promoter and signal sequence in the production of recombinant proteins in transgenic plants and transgenic plant seeds. In a claimed method, a transgenic monocot is obtained by transforming an immature embryo of the plant via Agrobacterium-mediated transforming an immature embryo of the plant via Agrobacterium-mediated transforming an immature embryo of the plant via Agrobacterium-mediated transformation with DNA comprising a plant alpha-amylase promoter (e.g. the rice alpha-Amy3-C promoter) that is induced under sugar-depleted or sugar-free conditions, a signal peptide sequence, and an exogenous sequence encoding a gene product; plant, which expresses the gene product under sugar-depleted or sugar-free conditions. The gene product may also be obtained by cultivating an angiosperm host cell. The transgenic monocot plants are especially useful in brewing and to produce glucose from starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-1992;
01-AUG-1995;
08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu S,
                                                                                                                                                                                                                                                                                                                                                                                                           Producing a transgenic monocot plant comprising a transgene under control of an alpha amylase promoter and signal peptide sequences, provides transgenic plants particularly cereals for the brewing industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
monocot; cereal; brewing.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 79-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-647191/74.
N-PSDB; AAI70540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice alpha-amylase (alpha-Amy3-C gene product).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NASC-) NAT SCI COUNCIL ROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
253 VNWVNAVGG 261
                  1 VNWVNKVGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu L,
                                                      Similarity
8; Conserv
                                                                                                            435
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0973324.
95US-0509962.
97US-0947201.
94US-0343380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chan M;
                                                                                                            ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0072917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide 26..428 
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                 82.1%;
                                                                                                                                                                                                                                                                                                                                                                                44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435
                                                      Score 46; DB pred. No. 14; 0; Mismatches
                                                                 DB 22;
                                                      1;
                                                                                Length 435;
                                                      Indels
                                                      0,
                                                      Gaps
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RESULT 5
AAB16272
ID AAB1
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AC AAB1
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DT 31-0
DT 91nu
XX
DE Pinu
XX
KW Euca
KW Plan
KW tran
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a gene expression system comprising the alpha-amylase gene promoter. DNA encoding the signal peptide of alpha-amylase and the promoter along with the glucuronidase reporter gene and hygromycin resistance gene are used in the construction of a GUS gene expression vector, which when transformed into rice suspension-cultured cells, can be used to investigate the expression of the vector under the control of the promoter. The gene expression system can be used to conduct gene regulation and protein expression and secretion using the characteristics of the alpha-amylase gene promoter and the DNA sequence encoding the signal peptide. The present sequence represents an alpha-amylase related protein used in the course of the present inventing.
                      Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic patransgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene expression system comprising the promoter region of alpha-amylase gene, produces large quantities of alpha-amylase in culture medium of sugar starved rice - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TW402638-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB97247 standard; Protein; 435 AA.
                                                                                                                                      Pinus radiata amylase
                                                                                                                                                                                             31-OCT-2000
                                                                                                                                                                                                                                                ААВ16272;
                                                                                                                                                                                                                                                                                                      AAB16272 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 12; 104pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-167365/17.
N-PSDB; AAH20285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-amylase related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB97247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NASC-) NAT SCI COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liou L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNWVNKVGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                VNWVNAVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97TW-0101436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97TW-0101436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter; expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 18;
                                                                                                                                                                                                                                                                                                      157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB Pred. No. 14; 0; Mismatches
                                                                                                                                      sequence SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                      pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 6
AAM50251
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                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
11-SEP-2001
                                                                                                                              Oryza sativa
                                                                                                                                                        monocot;
                                                                                                                                                                  Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
                                                                                                                                                                                            Rice alpha-amylase (alpha-Amy7-C gene product).
                                                                                                                                                                                                                        21-JAN-2002
                                                                                                                                                                                                                                                                           AAM50251 standard; Protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩PI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bloksberg LN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pinus radiata.
                         US6288302-B1
                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD (FLET-) FLETCHER CHALLENGE FORESTS
                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-339328/29.
                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                   VNWVNKVGGS 10
                                                                                                                                                         cereal;
                                                                                                                                                                                                                                                                                                                                           VNWINATGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                               157 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0170862
99US-0148426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-NZ00169
                                               /label= Signal_peptide
26..428
/label= Mature_protein
                                                                                                   Location/Qualifiers
                                                                                                                                                        brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHALLENGE FORESTS LTD.
                                                                                         . 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         80.4%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB Pred. No. 7; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157;
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                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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01-AUG-1995;
08-OCT-1997;
22-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium-mediated transformation with DNA comprising a plant alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that is induced under sugar-depleted or sugar-free conditions, a signal peptide sequence, and an exogenous sequence encoding a gene product; regenerating the transformed plant; and growing the transgenic plant, which expresses the gene product under sugar-depleted or sugar-free conditions. The gene product may also be obtained by cultivating an angiosperm host cell. The transgenic monocot plants are especially useful in brewing and to produce glucose from starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of rice (Oryza sativa) cv. M202 alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C (see AA170537). Expression of alpha-Amy7-C in cultured suspension cells of rice was induced 6-fold at day 12 after sugar depletion, and continued to increase up to day 14. The invention relates to the use of an alpha-amylase gene promoter and signal sequence in the production of recombinant proteins in transgenic plants and transgenic plant seeds. In a claimed method, a transgenic monocot is obtained by: transforming an immature embryo of the plant via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing a transgenic monocot plant comprising a transgene under control of an alpha amylase promoter and signal peptide sequences, provides transgenic plants particularly cereals for the brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-647191/74.
N-PSDB; AAI70537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YuS,
                                                                                                                                                                                                                                    AAB97245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
13-FEB-1992;
                            13-FEB-1992;
                                                                                      TW402638-A.
                                                                                                                                             Alpha-amylase;
                                                                                                                                                                          Alpha-amylase related protein #1.
                                                                                                                                                                                                       31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                              AAB97245 standard; Protein; 428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Column 61-64; 44pp; English.
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                                                         21-AUG-2000
                                                                                                                                                                                                                                                                                                                                       253 VNWVDRVGGA
                                                                                                                                                                                                                                                                                                                                                                   1 VNWVNKVGGS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu L,
                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0973324.
95US-0509962.
97US-0947201.
94US-0343380.
                                                                                                                                               promoter; expression vector; rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan M;
 97TW-0101436
                            97TW-0101436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0072917
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                                                                                                                                                                                                                                                                                                                                                                                                            80.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          DB
20;
                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 428
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RESULT 8

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DT 25-W

DT 12-J

XX

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KW Viru

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KW alph

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KW alph

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AN OBS:
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Best Local S
Matches 7
                                                   26-FEB-1988
26-FEB-1988
15-JUL-1988
17-FEB-1989
05-MAY-1989
08-JUN-1989
22-CCT-1990
16-JAN-1991
26-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a gene expression system comprising the alpha-amylase gene promoter. DNA encoding the signal peptide of alpha-amylase and the promoter along with the glucuronidase reporter gene and hygromycin resistance gene are used in the construction of a GUS gene expression vector, which when transformed into rice suspension-cultured cells, can be used to investigate the expression of the vector under the control of the promoter. The gene expression system can be used to conduct gene regulation and protein expression and secretion using the characteristics of the alpha-amylase gene promoter and the DNA sequence encoding the signal peptide. The present sequence represents an alpha-amylase related protein used in the course of the present numerican
                                                                                                                                                                                                                                                                                                                                                                                      Virus; recombination; plant virus; alpha trichosanthin; phenotype; alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus; rice necrosis virus tobamovirus; gene expression; chinese cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu S,
                                                                                                                                                                                                                                                                              31-MAY-1994.
                                                                                                                                                                                                                                                                                                                 US5316931-A.
                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR55130 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 8; 104pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene expression system comprising the promoter region of alpha-amylase gene, produces large quantities of alpha-amylase in culture medium of sugar starved rice.
                                                                                                                                                                                                                                           31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice alpha-amylase coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NASC-) NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-167365/17.
DB; AAH20283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 VNWVDRVGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VNWVNKVGGS 10
  BIOSOURCE GENETICS CORP
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428
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(first entry)
                                  88US-0160766

88US-01160771

88US-0219279

89US-0310881

89US-0341687

89US-034138

99US-036138

90US-0600244

91US-0747899

91US-0739143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB Pred. No. 20; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 9
AAR32987
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Best Local
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                                                               Donson J,
Grille LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant products; commercial production; fermentation; biosynthesis; natural products; recombinant proteins; product expression; protein expression; expressed proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The rice alpha-amylase gene may be inserted into a recombinant plant virus which can then be used to infect plants for the production of non-native products (in this case alpha-amylase). Other genes which may be inserted into the virus are those which control a phenotypic trait, such as male sterility, or sequences encoding anti-sense RNA which can be useful to prevent the expression of undesired phenotypic traits. The recombinant virus is derived from a plus sense, single stranded virus selected from tobamovirus, brome mosic virus, rice necrosis virus or a genthi virus.

(Updated on 25-MAR-2003 to correct PF field.)
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Turpen
                                                                                                                                                                                                                                                 (DAWS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant plant viral nucleic acid - capable of systemic infection and stable expression of non-native nucleic acid in
  WPI; 1993-076518/09
N-PSDB; AAQ37680.
                                                                                                                                                                                                                                                                                                                      01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09303161-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice alpha-amylase
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17-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR32987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Columns 53-56; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-176269/21.
N-PSDB; AAQ65574.
                                                                                                                                                                                                                              GARG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                 ) DAWSON W
) DONSON J.
) GARGER S
) GRANTHAM
) GRILLE L
) TURPEN A
) TURPEN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VNWVNKVGGS 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                          Dawson WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 AA;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.48;
                                                                                       Grantham GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB Pred. No. 20; 3; Mismatches
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                                                                                  Turpen
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                                                                                          Turpen AM,
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RESULT 10
AAW10469
JID AAW100
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XX 26-AP
XX 26-AP
XX Recom
KW Recom
KW tobac
XX Oryza
XX W0964
XX W0964
XX W0964
XX W0964
XX W0964
XX W0967
JU
XX W7-JU
XX WPI;
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is rice alpha amylase. The coding sequence was inserted into a recombinant plant viral nucleic acid which was then used to express a recombinant product (in this case rice alpha-amylase) in a plant. The plant viral sequence may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
                        A DNA sequence (AAT47095) codes for rice alpha-amylase (AAW10469). Movel viral nucleic acids can be constructed in which the alpha-amylase coding sequence is placed under control of the promoter of the tobacco mosaic virus coat protein gene, which has been deleted. The recombinant viral nucleic acid is capable of self-replication, encapsidation and systemic spread in infected tobacco plants, and directs expression of the alpha-amylase in plant
                                                                                                                                                                      Recombinant viral nucleic acid producing, e.g. male sterility in plants - comprises nucleic acid whose transcription is controlled
                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                              06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                 WO9640867-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus; TMV; rice; alpha-amylase; tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW10469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW10469 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maize streak viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant plant viral nucleic acids e.g. antibody or IL-1 in a plant
                                                                                                                               Example 4; Page 127-129; 149pp; English
                                                                                                                                                                                                                                                    Turpen
                                                                                                                                                                                                                                                                  Dawson
                                                                                                                                                                                                                                                                                          (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated
               tissue
                                                                                                                                                                                                                         1997-065181/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                    , MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                            AAT47095
                                                                                                                                                                                                                                                                                          BIOSOURCE TECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNWVDRVGGA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNWVNKVGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 AA;
                                                                                                                                                                                                                                                   Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                Donson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                    95US-0483502
                                                                                                                                                                                                                                                                                                                                              96WO-US09299
                                                                                                                                                                                                                                                    J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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70
                                                                                                                                                                                                                                                                Garger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB
Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                                                                                                                                                                                                SJ,
                                                                                                                                                                                                                                                                                            INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase; transgenic plant
                                                                                                                                                                                                                                                                  Grantham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  field.
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20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used to
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                                                                                                                                                                                                                                                                GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         express a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 434;
                                                                                                                                                                                                                                                                  Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                      controlled by
                                                                                                                                                                                                                                                                ĽK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prod.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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AAW11871
Вþ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1989;
08-JUN-1989;
31-JUL-1989;
26-FEB-1988;
26-FEB-1988;
15-JUL-1988;
22-OCT-1990;
16-JAN-1991;
26-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
       protein. These heterologous sequences are preferably under the control of the native promoter sequence. By using a plant virus existing cells can be altered with a new coding sequences without involving germ cell. The recombinant viruses are stable and can cause systemic infection, with stable expression/transcription in plants that are hosts for the non-native part of the vector. The plants that are hosts for the non-native part of the vector.
                                                             The sequences given in AAW11868-71 represent proteins which were produced by the recombinant viruses of the invention. The viruses are recombinant plant viruses which comprise a native plant virus subgenomic promoter, at least one non-native plant virus subgenomic promoter, and a sequence encoding a plant virus coat protein. These heterologous sequences are preferably under the control of the native promoter sequence. By using a plant virus
                                                                                                                                                                                                                                                                                               Dawson
Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subgenomic promoter; coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW11871
                                                                                                                                                                                                      Recombinant viral DNA for altering plant phenotype or protein prodn - contains non-native sub-genomic promoter for expression of heterologous protein and native promoter for expression of coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5589367-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-trichosanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW11871;
                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                    (BIOS-)
                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991;
                                                                                                                                                                                                                                                          1997-076845/07.
DB; AAT61377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 VNWVDRVGGA 268
                                                                                                                                                                                                                                                                                               AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNWVNKVGGS
                                                                                                                                                                                                                                                                                                                                    BIOSOURCE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                  4; Column 49-52; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434
                                                                                                                                                                                                                                                                                               Donson
Turpen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus; alpha-haemoglobin; human; chinese cucumber;
osanthin; rice; alpha amylase; beta-haemoglobin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first end
                                                                                                                                                                                                                                                                                                                                                                         90US-0600244.
91US-0641617.
91US-0737899.
                                                                                                                                                                                                                                                                                                                                                                                                             92US-0923692.
88US-0160766.
88US-0160771.
88US-0219279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0310881.
89US-0347637.
89US-0363138.
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                                                                                                                                                                                                                                                                                                                                                            91US-0739143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0184237
                                                                                                                                                                                                                                                                                               J,
TΗ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%;
                                                                                                                                                                                                                                                                                                           Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB Pred. No. 20; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                              Granthan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                              GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 434;
                                                                                                                                                                                                                                                                                                              Grill LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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nucleotide

sequences

encoding

these

protein

ector. The integrated

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RESULT 12
AAY01375
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  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                        17-FEB-1989;
05-MAY-1989;
08-JUN-1989;
31-JUL-1992;
19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in plant virus
protein gene.
(Updated on 29
(Updated on 29
                                                                                                                                                                                                                                26-FEB-1988
26-FEB-1988
15-JUL-1988
15-JUL-1988
22-OCT-1990
16-JAN-1991
26-JUL-1991
The invention relates to a recombinant plant viral nucleic acid derived from a plus sense, single stranded RNA plant virus. The recombinant plant viral nucleic acid comprises: (a) a first plant viral subgenemic promoter that is native to the plus sense, single stranded RNA plant virus and operably joined to a first nucleic acid expression sequence; and (b) a second plant viral subgenomic promoter that is non-native and is operably joined to a second nucleic acid expression sequence; where, (i) (a) and (b) are incapable of recombination with one another, (ii) either the
                                                                                                       Recombinant plant viral nucleic single stranded RNA plant virus products in a host
                                                                                                                                                                          Dawson
Turpen
                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-2003
04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                       US5889190-A.
                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                             transcription;
                                                                                                                                                                                                     (BIOS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sativa alpha-amylase
                                                                                                                                                       1999-243290/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
                                                                                                                                                                          , M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VNWVNKVGGS
                                                                                                                                                                                                     BIOSOURCE TECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNWVDRVGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434
                                                                                      Columns 47-51;
                                                                                                                                                                        Donson J,
Turpenth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            plant virus; coat protein; systemic infection;
n; therapeutic; rice; alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                      89US-0310881

89US-03463138

99US-0362138

92US-03623692

94US-0160766

88US-0160776

88US-0160771

88US-0210279

90US-0600244

91US-0737899

91US-0739143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA,
                                                                                                                                                                                                                                                                                                                                                  95US-0480432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
70
                                                                                                                                                                                   Garger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  either the
                                                                                     46pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB Pred. No. 20; 3; Mismatches
                                                                                                                                                                                   SJ,
                                                                                                                                                                                                      INC
                                                                                                                 acid derived from a plus sense,useful for the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF
                                                                                                                                                                                   Grantham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O-coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       field.)
field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                   GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 434;
                                                                                                                                                                                   Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the U1-coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                  of
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ARMSUAT 13
AAMSA4383
AID WAMSA4383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                         31-JUL-1992
26-FEB-1988
26-FEB-1988
15-JUL-1988
17-FEB-1989
05-MAY-1989
05-MAY-1989
22-OCT-1990
16-JUN-1991
26-JUL-1991
01-MG-1991
19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  first or the second nucleic acid expression sequence is a plant viral coat protein coding sequence. The recombinant plant viral nucleic acid allows the transcription of products in a host, such as therapeutic and other useful polypeptides or proteins e.g. enzymes, complex blomolecules and ribozymes. It also gives the option of applying the coding sequence to the desired organism, tissue, organ or cell, is stable for the foreign coding sequences and is capable of systemic infection in the plant host. The transformation and regeneration of target organisms become
                                                                                                                                                                                                                                                               Dawson
Turpen
                                                                                                         Recombinant plant viral vector - that is capable of systemic infection in host plant and stable production of heterologous DNA useful for producing therapeutic proteins for treating e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5866785-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice; alpha-amylase;
systemic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unnecessary.
(Updated on 20-MAR-2003 to correct PR field.)
                                                                Example 4; Columns 51-54; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW84383;
                                                                                                                                                                                                                                                                                                                                (BIOS-) BIOSOURCE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW84383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                 1999-142035/12.
DB; AAX03386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VNWVNKVGGS
||||::|||:
259 VNWVDRVGGA
                                                                                                                                                                                                                                                                  ΑM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 70. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 AA;
                                                                                                                                                                                                                                                               Donson
Turpen
                                                                                                                                                                                                                                                                                                                                                                         920S-0923692
880S-0160771
880S-0160771
880S-0160881
890S-0310881
990S-03108138
900S-036138
910S-0641617
910S-0641617
910S-0739143
940S-0739143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9505-0482920
                                                                                                                                                                                                                                                                  J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foreign gene expression; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
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70
                                                                                                                                                                                                                                                                                    Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 0%;
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Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                      Granthan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                      GL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 434;
                                                                                                                                                                                                                                                                                         Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter;
therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                         ĘĶ;
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The present sequence acid sequence can be

represents rice alpha-amylase expressed in the plant viral of

e. The nucleic constructs of

the

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RESULT 14
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Best Local
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                                                                                                                                                                                                               16-JAN-1991;
26-JUL-1991;
01-AUG-1991;
31-JUL-1992;
                                                                                                                                                                                                                                                                      26-FEB-1988;
15-JUL-1988;
05-MAY-1989;
22-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs.
                                           Recombinant non-retroviral nucleic acid for producing proteins such interleukins, melanin and vaccines, comprises subgenomic promoters linked to sequences coding for viral coat protein and heterologous proteins
                                                                                                                                                  Donson
                                                                                                                                                               Garger
                                                                                                                                                                                        (BIOS-)
                                                                                                                                                                                                                                                                                                                          08-JUN-1989;
26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                     17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    US6054566-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stereo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Animal RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY87792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY87792 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
            Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin;
                                                                                                          2000-338510/29
)B; AAA12394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sukin; EPO; erythropoietin; CSF; colony stimulating
VIII; hGH; human growth hormone; melanin; insulin;
specific catalysis; alpha-amylase; rice.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathbf{L}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                        BIOSOURCE TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNWVDRVGGA 268
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             Column
                                                                                                                                                               Grill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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8805-0160766

8805-0160771

8805-0160771

9005-0347637

9005-060424

9105-0641617

9105-0737899

9105-0737899

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9105-073899
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                                                                                                                                                             ĽK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral coat protein; plant; male sterility;
erythropoietin; CSF; colony stimulating fa
            65-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                             Turpen
           51pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 434;
                                                                                                                                                             Dawson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor;
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                                                                                                                                                             Turpen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 15
AAB12798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC This invention describes a novel recombinant viral nucleic acid (I) CC from a non-retroviral (+) sense, single stranded animal RNA virus CC comprising a nucleic acid sequence coding for a viral coat protein CC regulated by a native subgenomic promoter and other two heterologous CC nucleic acid sequences regulated by two other subgenomic promoters. (C nucleic acid sequences regulated by two other subgenomic promoters. (C nucleic acid sequences regulated by two other subgenomic promoters. (C nucleic acid sequences regulated by two other subgenomic promoters. (C neterility in plants. (I) is also useful for producing proteins such as content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the method of the method of the content of the method of the content of the method of the content of the method of the content of the method of the content of the method of the content of the method of the method of the content of the method of the method of the content of the method of the method of the content of the method of the method of the content of the method of the method of the content of the method of the content of the method of the content of the method of the method of the content of the content of the method of the content of the method of the content of the content of the method of the content of the content of the method of the content of the content of the method of the content of the content of the content of the method of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content
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Best Local
                                                                                                                                                                                                                                                                                               alpha-amylase gene, useful f product in a plant host cell
                                                                                                                                                                                                                                                                                                                        A gene expression system containing alpha-amylase gene, useful for mass
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1992;
04-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice; alpha-Amy6-C; alpha-Any7-C; alpha-Amy8-C; alpha-Amy10-C;
gene expression; promoter region; alpha-amylase; transgenic pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice alpha-Amy7-C protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB12798 standard; Protein; 428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-468171/41.
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                                                                                                                                                                                                                                                                                                                                                                                         AAA72947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNWVNKVGGS
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93JP-0297607.
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70.0%;
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Pred.
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                                                                                                                                                                                                                                                                                                                      the promotor region of production of a desired
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                                                                                                                                                                                                                                                                                                                          gene
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0;

the callus to roots and sprouts in a regeneration medium. The met be used for mass production of a desired gene product in a plant cell. The present sequence represents the rice alpha-Amy7-C prote which is used in an example from the present invention.

The method

The present invention describes a gene expression system containing the promoter region of an alpha-amylase gene. Also described is a method for preparing a transgenic rice plant comprising: (1) infecting Agrobacterium into an unmatured embryo of a rice plant; (2) simultaneously culturing the embryo with a suspended culture of a dicotyledon during the transforming step; (3) growing the transformed embryo to a callus in a selective medium containing a plant growth hormone; and (4) regenerating

Example 1;

Page 27-30; 39pp; Japanese.

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RESULT 16
AAR76520
                В
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                       genes.
NB. sc
                                                   AAR76519-R76521 represent the amylase gene products alpha-amylase-6-C, alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter regions of these amylase genes are used in a new gene expression system. The system may be used for the expression of heterologous genes in plant ceals and for the large scale production of the encoded products of such
                                                                                                                                                                                                                                                                                                                             /note=
Misc-difference 83
                                                                                                                                                                                                                                                                                                                                                                                         Alpha-Amy-6-C; amylase;
gene expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-amylase-7-C
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                    Claim 3; Page 27-30; 42pp; Japanese.
                                                                                                                  Gene expression system contg. alpha-amylase gene promoter in plants for expression of heterologous genes
                                                                                                                                                                                                04-NOV-1993;
                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                          WPI; 1995-236472/31.
N-PSDB; AAQ92806.
                                                                                                                                                                                  05-NOV-1992;
                                                                                                                                                                                                                  06-JUN-1995.
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                                                                                                                                                                                                                                                                                                                     Misc-difference
                Sequence
                               entered,
                                                                                                                                                                  (NASC-) NAT SCI COUNCIL
                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                     acids
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294
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233
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224
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218
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158
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262
                             in this sequence appear to table and the corresp. DNA
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70
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Pred. No.
Score
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42;
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                                                                                                                                                                                                                                                               CGT codon"
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                                                                                                                                                                                                                                                                                                             GAC
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62;
DВ
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16;
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file
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Length 429
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RESULT 17
ABB48004
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                     The present invention relates to the genome sequence of Listeria common copyrigenes EGD-e (see ABA03041). The genome sequence and fragments of the area useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein cc expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and cc for biosynthesis and biodegradation, especially biosynthesis of Vitamin cc B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication cc and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and cc vaccines compositions for the treatment or prevention of infections by L. CC monocytogenes and related organisms.

CC Note: The sequence data for this patent did not form part of the printed composition, but was obtained in electronic format directly from WIPO cc at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Deboux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart I Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Percez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypertides
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001; 2001WO-FR01118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes protein
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                                                                                                                                                                                                                                                                                                                                                                                   related polypeptides
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                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 709; 192pp; French.
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 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial infection;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      line; blosynthesis; blodegradation; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                     treatment
and
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Query Match Best Local Similarity

69.6%; 75.0%;

Score Pred.

39; DB 23; No. 70;

Length

Qγ

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RESULT 18
ABB49321
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Query Match
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                                                                                                                                 B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printe
                                                                                                                                                                                                                                                 monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, for biosynthesis and biodegradation, especially biosynthesis of Vitam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                 Sequence
                                                                                                                   specification,
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; SEQ ID No 2026; 192pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                    related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-010914/01
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                                                                                                                                                                                                                                                                                                                                                     it are useful
                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to the genome sequence of Listeria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides
 Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monocytogenes
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                                                                                                                                                                                                                                                                                                                                  EGD-e (see ABA03041). The genome sequence and fragments for selecting probes and primers for detecting genes in and related organisms, and for studying genetic
                                                                                                                   but was obtained in
               69.6%;
66.7%;
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Score 39; DB
Pred. No. 2.5e
2; Mismatches
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                                  DB 23;
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                                                                                                                     format
                                Length 548;
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                                                                                                                                                                   infections by L
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                                                                                                                                                                                                                                                     Vitamin
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RESULT 19
ABG66859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide that comprises a CC sequence with 60 % sequences (S1), given in specification, or a sequence CC polypeptide (PSP) sequences (S1), given in specification, or a sequence CC encoded by a nucleic acid comprising one of 114 prostate specific nucleic coid (PSNA) sequences (S2), given in specification. Also included are CC acid (PSNA) sequences (S2), given in specification. Also included are CC are proposed to the PSNA, a host cell comprising the vector. CC preparation of the PSP, a polypeptide encoded by the PSNA; an anti-PSP CC antibody the antibody or its fragment, a kit for detecting a risk of CC cancer or presence of cancer in a patient, comprising unit for CC cancer or presence of the PSP or the PSNA in a sample of a patient CC determining the presence of the PSP or the PSNA. The PSNA is useful for CC determining the presence of a prostate specific nucleic acid (PSNA) in a CC determining the presence of the PSP or the PSNA. The PSNA is useful for CC treating a patient with prostate specific nucleic acid (PSNA) in a prostate specific protein in a sample. The antibody is also useful for CC treating a patient with prostate cancer, where the administration of the cantibody induces an immune response against the prostate cancer cell antibody induces an immune response against the prostate cancer cell performs the psecond column of the PSNA in a cancer cell antibody induces an immune response against the prostate cancer cell performs the psecond column of the PSNA in a cancer cell antibody induces an immune response against the prostate cancer cell performs and column of the PSNA in a cancer cell antibody induces an immune response against the prostate cancer cell performs and column of the PSNA in a cancer cell antibody induces an immune response against the prostate cancer cell antibody induces an immune response against the prostate cancer cell performs and column of the PSNA in a cancer cell in the prostate cancer where the administration of the psNA in a cancer cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing the nucleic acid molecule or polypeptide. The PSP or the PSNA is useful for diagnosing and monitoring the presence and metastases of prostate cancer in a patient. The PSP is useful as a vaccine component for eliciting a humoral and/or cellular immune response, and for identifying an agonist and antagonist. The PSNA is used in gene therapy, identifying an agonist and antagonist. The PSNA is used in gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                         producing transgenic animals and cells, and for producing engineered prostate tissue for treatment and research. The PSNA is useful for detecting prostate cancer by detecting genetic lesions or mutations. PSP and the PSNA are useful for detecting, diagnosing, monitoring, staging and predicting cancers. The PSP and the PSNA are also useful
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diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate tissue. The present sequence is a prostate specific protein (PSP) sequence.
                                                                                                                                            identifying prostate tissue, and thus is useful in forensic science, prostate cell differentiation and development and in tissue engineering. The PSP, the PSNA and the antibody are useful for identifying,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 225-226; 248pp; English.
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herapy; vaccine;
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ous prostatic disease.
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RESULT 20
AAU65532
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypercosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the gresence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The polypeptides may be used as antipens in the production of antibodies compression and activity of P. acnes polypeptides and ctermining P. acnes proteins. These antibodies can be used as CC diagnostic agents for determining P. acnes presence, for example, by CC Note: The sequence data for this patient did not form part of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed content of the printed cont
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Best Local S
Matches 6
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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU65532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID No 26727;
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6; Conservative
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; 2000US-208841P.
; 2000US-216747P.
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75
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1069pp; English.
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Pred. No.
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34;
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RESULT 21
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The invention relates to constructing (M1) a strain of diploid fungal CC cells in which both alleles of a gene are modified, comprising modifying CC one allele by insertion or replacement; by a cassette having an expressible selectable marker and modifying other allele by CC recombination, of a promoter replacement fragment with a heterologous CC promoter, so that expression of the second allele is regulated by the CC promoter. (M1) is useful for constructing a strain of diploid fungal CC cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a threapeutic agent for treatment of a mammalian candisease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, signal transduction, DNA replication and cell division activity to inhibit growth or proliferation of C. ability to inhibit growth or proliferation of C. ability to inhibit growth or proliferation of C. ability and infection by C. albicans. The present sequence is that of an
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Best Local S
Matches 5
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20-FEB-2001;
22-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungus; yeast; tetracyclin; promoter; GRACE strain; blosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 44; SEQ ID NO 7931; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans.
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2001US-0792024.
2001US-314050P.
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Pred. No.
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ed. No. 58;
Mismatches
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Best Local
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14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

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RESULT 23
ABP56006
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       ABP56006 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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15-DEC-2000; 2000US-255839P
                                                                                                                                                      Chlamydia psittaci
                                                                                                                                                                                          Chlamydia; antibacterial; vaccine; immune response; infection
                                                                                                                                                                                                                               Chlamydia polypeptide SEQ ID NO 31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a vaccine (I) for the immunisation of an animal against Chlamydia psittaci comprising at least one polynucleotide (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is useful for the immunisation of a bovine. The present sequence represents a C. psittaci antigen from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia psittaci; vaccination; vaccine; antigen; immune response; immunisation; antibacterial; infection.
                                      17-DEC-2001; 2001WO-US48773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stemke-Hale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen CP4#13 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No. 2.2e.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                   232
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                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 232;
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RESULT 25
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AC ABU66
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DE C. p
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Vacc
KW Vacc
KW Comm
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                                                                                                                                                                                                                                                                                                                                Vaccine; chlamydia abortion; sexually community-acquired
                                                                                                                                                                                      16-AUG-2000;
                                                                                                                                                                                                                   17-DEC-2001; 2001US-0023437
                                                                                                                                                                                                                                                                           US2002183272-A1
                                                                                                                                                                                                                                                                                                    Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                       C. psittaci protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU66271 standard;
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New vaccine comprising Chlamydia antigen, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-Chlamydia species.
                                                                                                                              (STEM/)
                                                                                    Johnston
                                                                                                                                                          (JOHN/) JOHNSTON S A.
                                                      2003-328634/31.
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                                                                                                             ) STEMKE-HALE K.
) SYKES K F.
) KALTENBOECK B.
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                                         ABX99187.
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                                                                                    Stemke-Hale
                                                                                                                                                                                                                                                                                                                                transmitted disease; pneumonia; coronary
                                                                                                                                                                                                                                                                                                                                                             infection; blindness; mastitis; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                      from genomic DNA sequence CP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
75.0%;
a polynucleotide with a Chlamydia sequence or inducing an immune response against Chlamydia
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Pred. No. 2.2e
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                                                                                   Sykes KF,
                                                                                                                                                                                                                                                                                                                                ; atherosclerotic plaque; heart disease; antigen.
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                                                                                    Kaltenboeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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psitacci, Chlamydia pneumoniae, other Chlamydia species,
non-chlamydia infection -
                          Or.
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Claim 21; Page 55; 100pp; English

a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent for the first disease state/infectious agent, and testing the homology to see if it is an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide for the first disease state or infectious agent). The vaccine, antigens and polynucleotides are useful for inducing a protective immune response in vertebrate animals against C. psitacci, C. pneumoniae, other species of chlamydia, or a non-chlamydia infection. The antigens are also useful fo antibody preparation techniques. Chlamydia species are responsible for blindness, sexually transmitted disease, community-acquired pneumonia and act as co-factors in atherosclerotic plaque formation in coronary heart disease. C. psittaci in particular is a cause of mastitis infertility and abortion in cartile The present seminors is one of the the best immune response, and then expressing those clones in cell culture and purifying the protein), preparing antibodies against a Chlamydia antigen (comprising identifying a Chlamydia antigen that confers immune resistance against chlamydia bacterial infection when challenged with the Chlamydia species in which the antigen was prepared, generating an immune response in a vertebrate animal with the identified antigen, and obtaining antibodies produced in the animal, the antibodies are used to assay for the presence of chlamydia infection in a vertebrate animal) and testing for antigens for a first disease state/infectious agent (comprising determining an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent, obtaining a homologue of the antigenic polypeptide or the vector pcMV-Ubi(+P3). Also included are immunising an animal comprising providing to the animal at least one Chlamydia antigen or its antigenic fragment (expressed from the cloned polynucleotides) to induce an immune response (the proteins are chosen by transforming a vertebrate animal with constituents of the library and choosing those which elicit and at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen. The polynucleotide sequences are obtained from cloned expression library of fragmented genomic DNA (expressed in infertility and abortion in Chlamydia psittaci antigens invention relates to a vaccine comprising a pharmaceutical carrier ortion in cattle. antigens encoded The present sequence is one of the by a genomic DNA fragment of the

Matches Query Match Best Local : Sequence 3 WVNKVGGS Similarity 75.6; Conservative 232 AA 66.1%; 75.0%; Score 37; DB 24; Pred. No. 2.2e+02; Mismatches Length 232; Indels 0 Gaps

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RESULT 26 ABB53463 g Biosynthesis; Lactococcus ABB53463 standard; Protein; 12-OCT-2001 FR2807446-A1 Lactococcus 16-MAY-2002 180 WVDKAGGS 187 lactis lactis protein ybgB (first entry) biodegradation; lactic bacterium; yogurt; cheese IL1403 527

11-APR-2000; 2000FR-0004630

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RESULT 27
AAW88463
ID AAW88
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Best Local S
Matches 4
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Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-ocr-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                           New enzyme preparation comprising a xyloglucanase with an activity of 50 % at properties of cellulosic fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and linen fibres
                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1997;
07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus agaradhaerens xyloglucanase..
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                          Claim 18; Page
                                                                                                                                                                                                                                                                             Bjornvad ME,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus agaradhaerens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xyloglucanase; XEG1; detergent
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                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS.
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                                                                                                                                                                                                    I-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequence useful in the identification or Lactococcus {f tis} and {f related} species -
                                                                                                                                                                                                    1999-120866/10
DB; AAX06950.
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                                                                                                                                                                                                                                                                          Jorgensen PL,
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97DK-0000822
                            74-76;
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                       87pp; English
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                                                                                                                                                                                                                                                                          Outtrup
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Pred. No. 5
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RESULT 28
AAWOO383
ID AAWOO383
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N-PSDB;
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28-APR-1995;
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                                                                                                                                                1996-497624/49.
DB; AAT41849.
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95EP-0201115
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This polypeptide comprise alkaline xyloglucanase XEG1 of Bacillus agaradhaerens NCIMB 40482. The enzyme shows optimal cactivity at 50 deg C, and retains 20% of its activity at 50 deg C, and retains 20% of its activity in the pH craft for a control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
Cellulase with low ratio of tensile strength loss to antipilling properties - used in detergent composition which provides anti-greying, softening, anti-wrinkling and colour protection to fabrics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellulase; BCE 113; detergent; surfactant; laundry; tensile strength; antipilling.
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27..574
/label= Mat_protein
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detergent compsns."
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Pred. No. 5.3e
2; Mismatches
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es 2;
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Best Local
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              polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating discrete in the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conten
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                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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food supplement; medical ir
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23-AUG-2000;
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                                                                                                                                                                                                                                                     invention relates to isolated polynucleotide (I) and
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                   ID No 43657; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     j; gene mapping; gene therapy; forension imaging; diagnostic; genetic disorder
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  (I) and (II) are useful for sin expression or biological
expression
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5.7e+02;
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RESULT 30
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Best Local
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                          Claim 20;
                                                                                                                                                                                                                                                                                                       diagnostics, forensics, responsible for genetic
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Search completed: August 29, 2003, 18:44:01 Job time: 32.5714 secs
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                                                                                                                                                                                                                                                                                        responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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3    /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4    /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5    /cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-09-072-917A-9

Sequence 9, Applic Patent No. 628830; GENERAL INFORMAT

Application US/09072917A

ALIGNMENTS

INFORMATION:

APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair

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TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
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Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES:
                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: UZ-08/743.380
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NAME: BOrun, Michael F.
REGISTRATION NUMBER: 25447
                                                                                                                                                                                                                                                                                                                           STREET: Chicago
CITY: Chicago
TMATE: Illinois
TMATE: TMITTEE
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LENGTH: 428 amino acid
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLEFAX: 31.,
TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                         FILING DATE:
                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
REFERENCE/DOCKET NUMBER:
                    REGISTRATION NUMBER:
                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 VNWVDRVGGA 262
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6300 Sears Tower,
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              Michael F.
                                                                                                                                                     22-NOV-1994
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                                                                                                                                                                           US/08/343,380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4:
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Pred. No. 8
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,917A

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM:

60606

COUNTRY: CITY: Chicago STREET: ADDRESSEE:

Illinois : United States of America

E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower

MEDIUM TYPE:

Floppy disk

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

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253 VNWVNAVGG 261

1 VNWVNKVGG 9

US-09-072-917A-9

MOLECULE TYPE:

protein

TOPOLOGY: TYPE:

LENGTH:

amino acids

TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-AUG-1995

US 08/509,962

CLASSIFICATION: 800 FILING DATE:

REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

28123/34257

Best Local Similarity 88.9%; Matches 8; Conservative

0;

Mismatches

0;

Score 46; DB Pred. No. 5.8;

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Length 435 Indels

US-07-973-324A-4

Sequence 4, Application US/07973324A Patent No. 5460952

GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

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                                                                                                                                           ; MOLECULE TYPE: US-09-072-435-4
                                                                                                                                                                                                      PRIOR DATE: 27-ARK-1990
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ANTORNEY/AGENT INFORMATION:
NAME: GASS, DAVID A.
REGISTRATION NUMBER: 38,153
REFERENCEY/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
INFORMATION FOR SEO ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: 
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SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.4%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: APPRESS: MAISHALL, O'TOOLE, GETSTEIN, MUTTRY & BOTUN STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/639,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No.
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APPLICANT: Chan, Ming-Tsair
    Match 80.4%;
Local Similarity 70.0%;
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
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5215051
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                                                                                                                                                                                 protein
Score 45; DB:
Pred. No. 8.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28123/34274
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                                                                            DB 3;
0; Indels
                                                                       Length 428;
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Gaps
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TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4
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US-07-923-692C-6
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US-09-072-917A-4
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APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent NO. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                   Sequence 6, Application US/07923692C Patent No. 5316931
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/509,962
APILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REGISTRATION NUMBER: 38,153
                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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STATE: Illino:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                     Match 80.4%;
Local Similarity 70.0%;
les 7; Conservative
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253 VNWVDRVGGA 262
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Donson, Jon
Dawson, William 0.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Illinois
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                     Score 45; DB
Pred. No. 18.2;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 428;
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RESULT 7
US-08-184-237-6
US-08-184-237-6
; Sequence 6, Application US/08184237
; Patent No. 5589367
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
                                                                                                                                             뫄
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                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-07-923-692C-6
                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641
FILING DATE: 16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-JUL-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cli. CAL STATE: CAL 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 34 FILING DATE: 05-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Halluin, Albert P. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 10 FILING DATE: 26-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                Local Similarity les 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BIOG-20121
REFERENCE/DOCKET NUMBER: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   relephone:
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259 VNWVDRVGGA 268
                                                                                                                                                                             1 VNWVNKVGGS 10
                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                            434 amino acids
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2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                                                                                                  415-433-8716
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                             linear
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RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
                                                                                                                                                                                                                                   80.4%;
70.0%;
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                                                                                                                                                                                                                Score 45; DB 1
Pred. No. 8.4;
3; Mismatches
                                                                                                                                                                                                                                                    DB 1; Length 434;
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                                                                                                 , MOLECULE TYPE: protein US-08-184-237-6
                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                 TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent in Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 363,138 FILING DATE: 08-JUN-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 05-MAY-
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FILING DATE: 26-FEB-1980
PRIOR APPLICATION DATA:
US 160,771
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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STATE: C...
94111
                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 923,692 FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Limbach & Limbach STREET: 2001 Ferry Building CITY: San Francisco
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 15-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60 FILING DATE: 22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                 TOPOLOGY:
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   1 VNWVNKVGGS 10
                                 Similarity 7; Conserv
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Thomas H.
Muers
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                                 Conservative
                                                                                                                                   linear
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16-JAN-1991
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05-MAY-1989
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                                                80.4%;
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                                                                                                                                                                                                                                                                        28,957
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                                Score 45; DB:
Pred. No. 8.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                   DB 1;
                                   0;
                                                                Length 434;
                                   Indels
                                   0,
                                   Gaps
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259 VNWVDRVGGA 268

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TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Infear
MOLECULE TYPE: protein
US-08-482-920-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-482-920-6
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/482,921

PILING DATE: 07-JUNE-1955

PROOR APPLICATION NUMBER: US 184,237

PILING DATE: 19-JAN-1994

PRIOR APPLICATION NUMBER: US 600,244

APPLICATION NUMBER: US 600,244

PRIOR APPLICATION NUMBER: US 641,617

PRIOR APPLICATION NUMBER: US 641,617

PRIOR APPLICATION NUMBER: US 641,617
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APPLICANT: Donson
APPLICANT: Dawson
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APPLICATION NUMBER: US 310,881

FILING DATE: 17-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 160,766

FILING DATE: 26-FEB-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 160,771

FILING DATE: 26-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-MAY-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
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                                                                                                                                                                                    REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Application US/08482920 5866785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garger, Stephen J. Grill, Laurence K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donson, Jon
Dawson, William 0.
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                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1989
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  80.4%;
                                                                                                                                                                                                                                                                                                                                                                                       US 363,138
                                                                                                                                                                                                                                                                                                                                                                                                                                           US 347,637
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  Score 45;
Pred. No.
                                                                                                                                                                                                                                            8129-112
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  DB 2;
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RESULT 9
US-08-484-341-6
; Sequence 6, Application US/08484341
; Sequence 1, Application US/08484341
; GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William C
                                                                                              ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-484-341-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ър
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Query Match 80.4%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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GATGET, Stephen J.

GILL, Laurence K.

TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS: 1

CORRESPONDENCE ADDRESS: Limbach & Limbach

STREET: 2001 Ferry Building

CITY: San Francisco

STATE: CAL
                                                                                                                                                                                                                                       TELEPHONE: 415-433-4150
TELEPAX: 415-433-87.6
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE COMPATED SETTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENT IN PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENT IN DATA:

APPLICATION DATA:

APPLICATION UNBER: US/08/484,341

FILIMG DATE: O7-Un-1995

PRIOR APPLICATION UNBER: US/08/484,237

FILIMG DATE: CUNKNOWN>
APPLICATION NUMBER: US/08/244

FILING DATE: 22-CCT-1990

APPLICATION NUMBER: US/08/244

FILING DATE: 16-ZAN-1991

APPLICATION NUMBER: US/08/266

FILING DATE: 17-FEB-1990

APPLICATION NUMBER: US/07/66

FILING DATE: 26-FEB-1988

APPLICATION NUMBER: US/07/66

FILING DATE: 26-FEB-1988

APPLICATION NUMBER: US/07/167/71

FILING DATE: 26-FEB-1988

APPLICATION NUMBER: US/07/167/71

FILING DATE: 05-MX-1989

APPLICATION NUMBER: US/07/18/11

FILING DATE: 05-MX-1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

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APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989

APPLICATION NUMBER: US/07/1989
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-7UL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert p.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 VNWVDRVGGA 268
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                                                                                                                                                                                               TYPE: amino acid
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Score 45; DB 3; Length 434; Pred. No. |8.4; 3; Mismatches 0; Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
               TELEFAX: 202-962-8300
NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:

APPLICATION NUMBER: US 60
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                              FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                           FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2:
                                                                                                                                                                                                                                                                                                           FILING DATE: 26-FEB-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                         FILING DATE: 15-JUL-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 310,881 FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 6 FILING DATE: 16-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 VNWVDRVGGA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grill, Laurence K.
WENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grantham, George L.
Turpen, Thomas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turpen, Ann Myers
Garger, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Donson, Jon
Dawson, William O.
                                                        202-962-4810
                                                                                                                                                                                  US 219,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 600,244
                                                                                                                                                                                                                                     US 363,138
                                                                                                                                                                                                                                                                                              US 347,637
                                                                                                                                                                                                                                                                                                                                                US 160,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 641,617
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US-09-726-651A-6
                                                                                                                                                                                         RESULT 12
US-09-510-322A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR PEPLICATION NUMBER: 08/184,237
PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR FILING DATE: 1992-07-34
PRIOR FILING DATE: 1990-10-22
PRIOR FILING DATE: 1990-10-22
PRIOR FILING DATE: 1990-10-22
                                                                  Sequence 8, Application US/09510322A

Patent No. 6391557

GENERAL INFORMATION:

APPLICANT: Fox Chase Cancer Center

TITLE OF INVENTION: Nucleic Acid Encoding a Mismatch

TITLE OF INVENTION: Endonuclease and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6448046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DONSON, JON
APPLICANT: DAWSON, WI
APPLICANT: GRANTHAM,
APPLICANT: TURPEN, Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 008010023CNUS01
CURRENT APPLICATION NUMBER: US/09/726,651A
CURRENT FILING DATE: 2002-05-02
                  FILE REFERENCE: 9503dna CURRENT APPLICATION NUMBER: US/09/510,322A CURRENT FILING DATE: 2000-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TURPEN, Ann M.
APPLICANT: GARGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/737,899 PRIOR FILING DATE: 1991-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 07/641,617 PRIOR FILING DATE: 1991-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
  NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 434
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: CLONE: alpha-amylase OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 VNWVDRVGGA
                                                                                                                                                                                                                                                                        259 VNWVDRVGGA 268
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                                                                                                                                                                                                                                                                                                            1 VNWVNKVGGS 10
SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09726651A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRANTHAM, GEORGE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TURPEN, Thomas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAWSON, William O.
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                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                       80.4%;
70.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 4; Length 434; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                       Mismatches
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8.4;
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US-09-110-959A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-24308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-252-991A-24308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Plant
US-09-510-322A-8
                                                       CÜRRENT APPLICATION NUMBER: US/09/110,959A
CÜRRENT FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 0822/97
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/054,039
PRIOR APPLICATION NUMBER: 60/063,694
PRIOR APPLICATION NUMBER: 60/063,694
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
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Patent No. 6551795
GEMERAL IMPORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND MAINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 24308
LENGTH: 460
TYPET: DEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09110959A Patent No. 6268197
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                          SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
APPLICANT: Jorgensen, Per Lina
APPLICANT: Bjornvad, Mads Eskelind
APPLICANT: Bjornvad, Mads Eskelind
TITLE OF INVENTION: Alkaline Xyloglucanase
FILE REFERENCE: 5206.200
LENGTH: 537
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55. es 5; Conservative
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407 VTWLTEVGGS 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 4; Length 460; Pred. No. 1.7e+02; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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US-09-107-532A-4136
RESULT 16
                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                               132 DWVSKFGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...544
SEQUENCE DESCRIPTION: SEQ ID NO: 4136:
US-09-107-532A-4136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bacillus agaradhaerens NCIMB 40482
US-09-110-959A-4
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION UNMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: GO-085,598
PRIOR APPLICATION DATA: 30-Jun-1998
PRIOR APPLICATION UNMBER: 60/085,598
APPLICATION NUMBER: 60/051571
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
NAME: ARINI-6110, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION THOORMATION:
TELEPHONE: (781)893-5007
TELEFAN: (781)893-8277
INFORMATION FOR SEQ ID NO: 4136:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4136, Application US/09107532A Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.1%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VTWQNQMGGS 71
                                     2 NWVNKVGGS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VNWVNKVGGS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Beaver Street
140
                                                                         66.1%; Score 37; DB 4; 66.7%; Pred. No. 2e+02; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 3; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and David Bush AND AMINO ACID SEQUENCES RELATING TO FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                 Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 537;
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                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                           Gaps
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US-08-732-433-1
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TITLE OF INVENTION: No. 6063611el Alkaline Cellulase and
TITLE OF INVENTION: Method of Production Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer of Camaranteer
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APPLICANT:
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FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
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CTTY: Palo Alto
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CORRESPONDENCE ADDRESS:
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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REGISTRATION NUMBER: 35,69
REFERENCE/DOCKET NUMBER: G
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OPERATING SYSTEM:
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COMPUTER:
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Van Beckhoven, Rudolf Franciscus Wilhelmus Cornelis
                                                                                                                   U.S.A.
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IBM PC compatible
                                                                                                                                                                                                                                                Henkel Corporation
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Pred. No. 2.
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2.1e+02;
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US-09-107-532A-5530
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mulphy, Glenn E. J.
REGISTRATION NUMBER: 33,539
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APPLICATION NUMBER: PC1/-
TING DATE: 26 Apr. 1996
TING DATE: 26 Apr. 1996
TING DATE: 27 Apr. 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 95201115.
FILING DATE: 28 Apr. 1995
APPLICATION NUMBER: U.S. 614,115
FILING DATE: 12 Mar. 1996
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SOFTWARE: MS Word
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                                                                                                                                  COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOETWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
TELECOMMUNICATION INFORMATION:
                                          ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, PameJ
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                       APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
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                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02354
                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
              REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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50.0%;
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                                          Pamela Deneke
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INAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...427
SEQUENCE DESCRIPTION: SEQ ID NO: 5530:
US-09-107-532A-5530
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US-07-973-324A-2
                                                                                                         US-07-973-324A-2
                                                                                                                                  APPLICATION NUMBER: US/07/973

APPLICATION NUMBER: US/07/973

ETILING DATE: 04-NOV-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BOTUN, MICHAEL F.

REGISTRATION NUMBER: 25447

REFERENCE/DOCKET NUMBER: 31149

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEPHONE: 312/474-6300

TELERX: 32/474-04

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 438 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids
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Best Local
                               Query Match
Best Local Similarity
Matches 6; Conserv
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5530:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, L1-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase G
NUMBER OF SEQUENCES: 7
OURRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 s
CITY: Chicago
STATE: Illinoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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5. 5460952
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1 VNWVNKVGG 9
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                                   Conservative
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                                                                                                                      protein
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ower, 233 South Wacker Drive
                                 Score 36; DB
Pred. No. 2.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                       31149
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                                                  DB 1;
2.3e+02;
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                                 3; Indels
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                                                                   Length 438;
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US-09-072-435-2
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Patent No.
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Best Local :
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RESULT 20
US-08-343-380-2
US-08-62-2
; Sequence 2, Application US/08343380
; Patent NO. 5712112
; GENERAL INFORMATION:
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COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/343,380
FILING DATE: 22-NOY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION UMBER: 35447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION I
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                      APPLICANT: Liu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING TH
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TODOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Gene Expression System Comprising the TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
STREET: 233 So
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                   No. 6215051
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66.7%;
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3;
                                                                                                                                                                                         COMPRISING THE ALPHA-AMYLASE GENES
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RESULT 22
US-09-072-917A-2
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transtitle OF INVENTION: Plant Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application Patent No. 6288302 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/3427.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING XSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity les 6; Conserv
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                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                    APPLICATION NUMBER: US/09/072,917A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 VNWAQAVGG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09072917A
                                                                                                                                                                                                                                                                  E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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                800
                                                                                                                                                                                                                                                                                                                            Plant Seeds
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                                                                                            Recombinant Proteins in Transgenic Plants and Transgenic
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Pred. No. 2.3e+02;
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RESULT 24
US-08-983-607-47
; Sequence 47, A
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Best Local Similarity
Watches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-527-236A-26
                                                              sequence 47, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09527236A Patent No. 6358508
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ni, Jian APPLICANT: Yu, Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312) 474-04/
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
              APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION:
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                                                                                                                                                                                               35 IKWVNKTG 42
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6; Conserva
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312) 474-0448
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bodies
                Human Anti-Tumor Monoclonal Anti-
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Pred. No.
                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
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2.3e+02;
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US-08-818-112-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PCT/IB96/01032

PILLING DATE: JUNE 28, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MATY M. KILDSKY 203

REFERENCE/DOCKET NUMBER: 32423

REFERENCE/DOCKET NUMBER: 00R-679

TELECOMMUNICATION INFORMATION:

TELEPHONE: 203-773-1183

INFORMATION FOR SEO ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 residues

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
                                                                                                        Sequence 66, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.5%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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DESCRIPTION: polypeptide
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SOFTMARE: WORD PROCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91
FILING DATE: April 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS: Department of Molecular Biophysics
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
REPLICANT: Skeiky Vasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: "Yeardatk, Daniel R.
APPLICANT: "Twardatk, Daniel R.
APPLICANT: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ITITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: E26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lympho-INDIVIDUAL ISOLATE: cytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 266 Whit
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: United States of America
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Pred. No.
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RESULT 26
US-08-818-111-67
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Best Local :
COMPUTER READALE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPUTER: 1BM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 7
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY_AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven ...
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Canpos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 13-MAI
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linear
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Pred. No.
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                                                                                                                                                                                                                                                                                 701 Fifth Avenue
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le+02;
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RESULT 28
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                             TELEFAX: (206) 682-60: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/056,556 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPPRADED. PARTY PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                            110
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                                                                         1 VNWVNKVGGS 10
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                                                                                                       Similarity 6; Conserv
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                                                                                                       Conservative
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NO: 66:
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                                                                                                      Score 35; DB
Pred. No. le+C
1; Mismatches
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Pred. No. 1e+(
1; Mismatches
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1e+02;
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1e+02;
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                                                                                                                                    Length 132;
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                                                                                                                                                                                                                                                                          RESULT 29
US-09-333-593A-4
                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                       Sequence 4, Application US/09333593A Patent No. 6313269
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                             APPLICANT: TRUNEH, ALEMSEGED TITLE OF INVENTION: TUMOR NEC TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/333,593A CURRENT FILING DATE: 1999-06-15 PRIOR APPLICATION NUMBER: 08/916,625 PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-490
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             110 VNWQTKSGGT 119
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                                                                                                                                    MARSHALL, LISA A. ROSHAK, AMY K. TAN, KONG B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                       YOUNG, PETER F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                     PETER R
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                                                                                                      TUMOR NECROSIS FACTOR RELATED RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%;
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210121.41709
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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COUNTRY USA

ZIP: 98104-7092

COUNTRY USA

COMPUTER EADABLE FOOM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOUTWARR: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,112

FILING DATE: 13-MAR-1997

CLASSIFICATION UNBER: 31,392

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C6

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENCTH: 355 amino acids

STRANDEDNESS: single

US-08-818-112-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Ekelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Houghton, Raymond

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: TWARDZING COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 303
                                                            Query Match 62.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 CONTY: Seattle STATE: Washing
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1 VNWVNKVGGS 10
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6290969
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                                                            Score 35; DB 3; Length 355; Pred. No. 2.8e+02; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 4; Length 303; Pred. No. 2.4e+02; Indels 1; Mismatches 2; Indels
                                                              0;
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o 333 VNWQTKSGGT 342

Search completed: August 29, 2003, 18:44:41 Job time: 11.5714 secs

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Title: Perfect score: Sequence:

Run

protein 9

Scoring table:

Minimum Maximum

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 :
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Match
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2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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56
1 VNWVNKVGGS 10
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Gapop 10.0 , Gapext 0.
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4. //cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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            US-10-280-679B-6
US-10-1001-870-167
US-10-1001-870-167
US-10-156-761-19047
US-10-156-761-7974
US-10-156-761-7974
US-10-156-761-7974
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US-10-23-63-5
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US-10-156-7477B-2
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US-09-815-761-9313
US-09-756-854-26
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    Sequence 6, Appli
Sequence 157, App
Sequence 13047, Ap
Sequence 37, Appli
Sequence 2, Appli
Sequence 33, Appl
Sequence 434, Appl
Sequence 51, Appl
Sequence 212, Appl
Sequence 212, Appl
Sequence 144, Appl
Sequence 13987, A
Sequence 13987, A
Sequence 9313, Appl
Sequence 14, Appl
Sequence 26, Appli
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    Sequence 26, Appl
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Sequence 11, App1
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Result No.

Score

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RESULT 2
US-10-001-870-167
US-10-001-870-167
; Sequence 167, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
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US-10-280-679B-6
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Publication No. US20030150019A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-0109-US03
FOLD REPUBLICATION NUMBER: US/10/280,679B
CURRENT FILING DATE: 2000-10-24
CURRENT FILING DATE: 2000-10-24
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PRIOR FILING DATE: 1995-06-07
PRIOR PPLICATION NUMBER: 07/923,692
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR PILING DATE: 1991-01-16
PRIOR PILING DATE: 1991-07-26
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
PRIOR APPLICATION NUMBER: 07/739,143
PRIOR FILING DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/310,881
PRIOR PILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 07/310,766
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR FILING DATE: 1988-02-26
PRIOR FILING DATE: 1988-02-26
PRIOR FILING DATE: 1988-02-26
                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                     Matches
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Best Local
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PRIOR FILING DATE: 2000-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 07/160,771 PRIOR FILING DATE: 1988-02-26
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                                                                                                                                                                                                                                                                                                                                                     LENGTH: 434
                                                                                                                                                                     259 VNWVDRVGGA 268
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                                                                                                                                                                                                                                   Similarity 7; Conserv
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5 US-10-175-902-2

5 US-10-060-036-164

4 US-10-016-634A-175

5 US-10-156-761-8095

1 US-09-815-242-13226

1 US-09-845-258-18

1 US-09-845-258-18

1 US-09-842-464A-2

1 US-09-842-464A-2

1 US-09-842-464A-2

1 US-09-842-464A-3

5 US-10-184-485-3

5 US-10-217-613-3
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Pred. No. 9.9;
3; Mismatches C
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Sequence 164, App
Sequence 167, App
Sequence 175, App
Sequence 1325, Ap
Sequence 18, Appli
Sequence 6, Appli
Sequence 2, Appli
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Best Local
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                                    APPLICANT:
     APPLICANT:
                    APPLICANT:
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13047
                                                                                                                                            RESULT 4
US-10-156-761-7974
US-10-156-761-7974, Application US/10156761
; Sequence 7974, Application US/10156761
; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Streptomyces US-10-156-761-13047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapien US-10-001-870-167
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US-10-156-761-13047
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes
FILE REFERENCE: DEX-0283
CURRENT APPLICATION NUMBER: US/10/001,870
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 167
LENGTH: 54
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISKIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                        GENERAL INFORMATION:
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                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
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43 INWVNLVG 50
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SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                        ISHIKAWA, JUN
HORIKAWA, HIROSHI
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75.08;
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71.4%;
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Pred. No. 19;
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TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC ACID TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA FILE REFERENCE: UTSD:736US CURRENT APPLICATION NUMBER: US/10/023,437 CURRENT FILING DATE: 2001-12-17 PRIOR APPLICATION UNMBER: 60/225,839 PRIOR APPLICATION UNMBER: 60/225,839 PRIOR FILING DATE: 2000-12-15 NUMBER OF SEQ ID NOS: 69 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 31

LENGTH OF SEQ ID NOS: 69 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                         RESUL7 6
US-09-863-547B-2
; Sequence 2, Application US/09863547B
; Patent No. US20020128166A1
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US-10-023-437-31
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; ORGANISM: Chlamydia psittaci
US-10-023-437-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7974
LENGTH: 153
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local
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Publication No
                                                                                    APPLICANT: Henkel KGaA
APPLICANN: Hermanus, Lentus B. M.
APPLICANI: Van Beckhoven, Rudolf F.
APPLICANI: Wanurer, Karl-Heinz
APPLICANI: Kottwitz, Beatrix
APPLICANI: Weiss, Albrecht
APPLICANI: Weiss, Albrecht
APPLICANI: Van Solingen, Pieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEWKE-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-252
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
CURRENT APPLICATION NUMBER: US/09/863,547B CURRENT FILING DATE: 2002-02-13
                                              RAPLICANT: Van Solingen, Pieter
TITLE OF INVENTION: Detergents Comprising Cellulases
FILE REFERENCE: H 1920 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0%; es 6; Conservative
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180 WVDKAGGS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 14; Length 232; Pred. No. 1.1e+02; 1; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 08/945,574
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION UMBER: PCT/EP96/01755
PRIOR FILING DATE: 1996-04-26
PRIOR PPLICATION UMBER: US 08/614,115
PRIOR APPLICATION NUMBER: EP 95201115.3
PRIOR APPLICATION NUMBER: EP 95201115.3
PRIOR TILING DATE: 1995-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTION OF SEQ ID NOS: 2
SOFTWARE: PATENTION OF SEQ ID NOS: 2
LENGTH: 574
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US-10-023-437-33
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US-09-863-547B-2
Sequence 434, Application US/10080170

Publication No. US20030129601A1

GENERAL INFORMATION:

APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 500/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: SYEMKE-HALE, KATHERINE
APPLICANT: SYEMKE-HALE, KATHERINE
APPLICANT: SYEES, KATHERINE
APPLICANT: RALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC /
TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC /
TITLE REFERENCE: UTSD:736US
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 50/225,839
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2001-12-15
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2001-12-15
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2001-12-15
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2001-12-15
PRIOR APPLICATION NUMBER: 60/225,839
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Publication No. US20020183272A1
GENERAL INFORMATION:
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Best Local Similarity 50.0

Matches 5; Conservative
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Best Local S
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TYPE: PRT
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Local Similarity 75.0%;
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 WVDKAGGS 381
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TYPE: PRT GRGANISM: Mycobacterium tuberculosis US-10-080-170-434
                                                           APPLICANT: Kerovuo, Janne S.
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
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; Sequence 51, Application No. US20; Publication No. US20; GENERAL INFORMATION:
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Best Local
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Best Local
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TITLE OF INVENTION: Self-processing Plants and Plant Parts
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 60
                             PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
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NO 212
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                FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                    Frey, Gerhard
Short, Jay M.
Mathur, Eric J.
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                                                                                                                                                                                                                                                                                     Gray, Kevin A.
                                                                                                                                                                                                                                                                                                                                                          Richardson, Toby
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Pred. No. 1.1e+02;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: VARIANT
; LOCATION: 462
; OTHER INFORMATION: Xaa = Gly
US-09-967-4778-2
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US-09-815-242-13987
                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                 Sequence 13987, Application US/09815242 Patent No. US20020061569A1
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APPLICANT:
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APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4,
TITLE OF INVENTION: FAT7
                                                                                               TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                 APPLICANT:
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PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                 Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                  Wall, Daniel
                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                 Carr, Grant J.
                                                                                                                                                                                                   Trawick, John D.
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85.7%;
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60.0%;
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Pred. No.
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Pred. No.
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3.5e+02;
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APPLICANT: SAKAI, Takeshi
APPLICANT: KATO, Ikunoshin
ITILE DE INVENTON: ALPHA-BAGRASE AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: TOMONO-1
CURRENT APPLICATION NUMBER: US/09/924,097
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: JP00/00966
PRIOR APPLICATION NUMBER: 11-44890
PRIOR APPLICATION NUMBER: 11-44890
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 30
SOSTWARE: PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATENTIAN PATE
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PRIOR FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FASTSEO FOR WINDOWS Version 4.0
SEO ID NO 13987
LENGTH: 550
TYPE: PRT
RESULT 14
US-10-156-761-9313
Sequence 9313, Application US/10156761
Publication No. US20030119018A1
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; LOCATION: (1)...(550)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-815-242-13987
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US-09-924-097-14
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Best Local Similarity
Matches 6; Conserva
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APPLICANT: NOMURA, Yoshiko
APPLICANT: SAGAWA, Hiroaki
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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FEATURE:
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                                                                                                                                                                                                                        378 NWVNQVQG 385
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 10; Length 925; Pred. No. 6.1e+02; l; Mismatches 1; Indels
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GENERAL INFORMATION:

APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHKAWA, JUN
APPLICANT: HORIKAWA, JINOSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
ATTILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-756-854-26
US-09-756-854-26
Sequence 26. Application US/09756854
Patent No. US20020164684A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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TYPE: PRT
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/095,094

ATTORING DATE: «Unknown»

ATTORINEY/AGENT INFORMATION:

NAME: HOOVET, Kenley K.

REGISTRATION NUMBER: 40,302

REGISTRATION NUMBER: P375

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:
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es 5; Conserv
                                                                                                                                                                                                                                                                                  ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ni, Jian
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              684 NWLNKLG 690
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71.48;
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Pred. No. 6
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6.3e+02;
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-756-854-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gentz, Reiner L.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1

CURRENT APPLICATION NUMBER: US/10/041,574

CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR APPLICATION NUMBER: 09/055,094
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR APPLICATION NUMBER: 09/095,094
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PRIOR APPLICATION NUMBER: 09/095,094
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-26
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US-09-759-143-819
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Xu, Jiang
APPLICANT: Dillon, II
APPLICANT: Mitcham,
APPLICANT: Harlocker
APPLICANT: Hang, Xt,
APPLICANT: Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Yu, Guo:
APPLICANT: Fan, Pir
                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/134,220 PRIOR FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 27
                                                                          APPLICANT:
                                                        APPLICANT:
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nes 5; Conserv
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5; Conserva
                                                     Fanger, Gary R. Retter, Marc W. Stolk, John A.
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Fan, Ping
Day, Craig H. Vedvick, Thomas S. Carter, Darrick
                                                                                                                Kalos, Michael D.
                                                                                                                                   Henderson,
                                                                                                                                                   Jiang, Yuqui
                                                                                                                                                                                        Mitcham, Jennifer L.
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62.5%;
                                                                                                                                   Robert A.
                                                                                                                                                                       Susan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
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RESULT 19 US-09-780-669-819 ; Sequence 819, Application US/09780669

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APPLICANT: Li, Samuer
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hapler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 819
LENCTH: 132
TYPE: PRT
ORGANISM: Homo sapien
US-09-759-143-819
62.5%; Score 35; DB 9; Length 132;
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Best Local Similarity
Watches 6; Conserve
                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ FOR
SEQ ID NO 848
LENGTH: 132
LENGTH: 132
                                                                                                                                 ; ORGANISM: Homo sapiens US-09-759-143-848
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 848, Application US/09759143 Patent No. US20020022248A1
                                                             Best Local
Matches
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Best Local :
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT EPPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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110 VNWQTKSGGT 119
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                 1 VNWVNKVGGS 10
                                                               Similarity 60. 6; Conservative
                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
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                                                                                62.5%;
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                                                                               Score 35; DB 9;
Pred. No. 1.4e+02;
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                                                                    Mismatches
                                                                                                Length 132;
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APPLICANT: MCNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows ...
SEQ ID NO 819
LENGTH: 132
TYPE: PPT
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US-09-780-669-848
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Patent No. US20020051977A1
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Best Local :
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
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Local Similarity 60.0%;
hes 6; Conservative
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Hang, Aijun
Skelky, Yasir A.W.
Hepler, William
Hural, John
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Retter, Marc W.
Stolk, John A.
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Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                         Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                               Li, Samuel
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Kalos, Michael
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                                                                                                                                                                                                                                                                                                                                               Harlocker, Susan L.
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Mitcham, Jennifer L.
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                                                                                                                                                                                                                                                                                                             Robert A.
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Pred. No. 1.4e+02;
1; Mismatches 3;
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CURRENT FILING DATE: 200
NUMBER OF SEQ ID NOS: 94
SOSTWARE: FastSEQ for W1
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-848
                                                                                                                                                                                                                                                                   RESULT 22
US-09-822-827-848
US-09-822-827-848
; Sequence 846, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE REFERENCE: 21021.534C1
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US-09-822-827-819
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Patent No. US20020081680A1
GENERAL INCORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 819
SEQ ID NO 819
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Best Local Similarity bu..
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Matches 6
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CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
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Matches 6
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TYPE: PRT
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nes 6; Conserv
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110 VNWQTKSGGT 119
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Pred. No. 1.4e+02;
1; Mismatches 3;
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Pred. No. 1.4e+02;
1; Mismatches 3
                                                             Score 35; DB 9; Le
Pred. No. 1.4e+02;
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RESULT 24
US-09-895-793-848
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 819
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                          APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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TYPE: PRT
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
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Kalos, Michael D.
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Kalos, Michael D.
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Vedvick, Thomas S.
                                       Skeiky, Yasir A.W.
Hepler, William T.
                                                                         Wang, Aijun
                                                                                                       Carter, Darrick
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                            Henderson, Robert A.
                                                                                     Li, Samuel X.
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Patricia D
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Pred. No. 1.4e+02;
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110 VNWQTKSGGT 119

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Query Match
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                                                                                       ; TYPE: PRT; ORGANISM: Homo sapien US-09-895-814-819
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-848
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                                                                                                                              APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C26

CURRENT APPLICATION UNMERR: US/09/895,814

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 990

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 819

LENGTH: 132
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NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 848
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Best Local
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIACNOSIS OF PROSTATE CANCER
EILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
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1 VNWVNKVGGS 10
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Vinals de Bassols, Carlota
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Vinals de Bassols, Carlota
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Carter, Darrick
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Hepler, William T.
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Kalos, Michael D.
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Pred. No. 1.4e+02;
                                          Score 35; DB 10;
Pred. No. 1.4e+02;
                              Mismatches
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RESULT 26 US-09-895-814-848

Sequence 848, Publication No.

INFORMATION:

Jiangchun

APPLICANT: APPLICANT:

Jiang, Yuqiu Kalos, Michael D.

Retter, Marc W.

Vedvick, Thomas S. Carter, Darrick Li, Samuel X.

Aijun

John

Craig H.

John A.

PPLICANT:

Teresa

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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C26

CURRENT APPLICATION NUMBER: US/09/895,814

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 990

SOFTWARE: FASTSEQ FOR Windows Version 3.0

SEQ ID NO 848

LENGTH: 132
                                          CORRESPONDENCE ADDRESS:

ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                               Hendrickson, Robald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Mitcham, Jennifer L.
Harlocker, Susan L.
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Hepler, William T.
Henderson, Robert A.
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o. US20020193296A1
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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Dillon, Davin C.
Campos-Neto, Antonio
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US-10-193-002-67
; Sequence 67, Applicatio
; Publication No. US20030
; GENERAL INFORMATION:
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TYPE: amino acids
STRANDENNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-084-843-86
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APPLICATION NUMBER: US/09/072,967

APPLICATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: MAKI, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

INFORMATION FOR SEQ 1D NO: 66:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
          CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION DATA:
CLASSIFICATION DATA:
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ZIP: 98104-7092

COMPUTER RRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                  Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESSE
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
PRIOR APPLICATION DATA:
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No. US20030135026A1
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Dillon, Davin C.
Campos-Neto, Antonia
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110 VNWOTKSGGT 119

1 VNWVNKVGGS 10

NUMBER OF SEQUENCES:

CITY: Seattle STATE: Washington

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-895-814-848

Query Match Best Local S

Match 62.5%; Local Similarity 60.0%; es 6; Conservative

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1 VNWVNKVGGS

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US-10-144-678A-819
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                                                         ; TYPE: PRT; ORGANISM: Homo sapiens US-10-144-678A-819
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Best Local Similarity
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SEQ ID NO 819
LENGTH: 132
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APPLICANT: D1
APPLICANT: M1
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Query Match 62.9
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/144,678A CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
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LENGTH: 132 amino acids
TYPE: amino acid
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Retter, Marc W.
Stolk, John A.
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
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Hepler, William T.
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Li, Samuel X.
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Score 35; DB 12;
Pred. No. 1.4e+02;
1; Mismatches 3
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Pred. No. 1.4e+02;
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                            Length 132;
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Search completed: August 29, 2003, 18:47:49
Job time: 17.7143 secs
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                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-10-144-678A-848
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Best Local S
Matches 6
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
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                                                                                                                                                                                                                                                                                       APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 2101.21.427028
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
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Hepler, William T.
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60.0%;
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Pred. No. 1.4e+02;
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Title:
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Listing first 100 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      protein search, using sw model
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
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Gapop 10.0 , Gapext 0.5
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     VNWVNKVGGS 10
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ALIGNMENTS

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alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Hordeum vulgare (barley) C;Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999 C;Accession: JE0406; B30759; S06275; B31960; B21826 R;Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan Plant Mol. Biol. 12, 119-121, 1989 A;Title: Nucleotide and predicted amino acid sequences of two different genes for high-FA;Reference number: JE0405 A;Accession: JE0406
A;Pathway: glycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: aleurone cell; germination; glycosidase; hydrolase;
F;172-318/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 379-389, T, 391-392, D, 394-429 <HUA>
A; Residues: 379-389, T, 391-392, D, 394-429 <HUA>
A; Cross-references: GB: K02636; NID: g166992; PIDN: AAA32932.1; PID: g166993
A; Experimental source: CV. Himalaya aleurone cell mRNA (clone 96 for alp C; Genetics: A56>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain Himalaya gene Amy46 for alpha-amylase R;Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S. J. Mol. Appl. Genet. 2, 579-588, 1984
A;Reference number: A92837; MUID:85159405; PMID:6335720
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A;Title: Barley alpha-amylase genes. Quantitative comparison A;Reference number: A92700; MUID:89066691; PMID:3264283
A;Accession: B31960
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A; Title: Structure and organization of two divergent alpha-amylase A; Reference number: S06275
A; Accession: S06275
                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 29/3; 346/3
C; Genetics: <A46>
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A; Residues: 1-51 <KHU>
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J. Biol. Chem. 263,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cv. Sundance gene for alpha-amylase 1 precursor
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A;Residues: 1-11,'LI',14-32,'S',34-57,'I',59-79,'Y',81-139,'R',141-160,'PA',163-164,'R'
A;Cross-references: EMBL:M17125; NID:g166978; PIDN:AAA32926.1; PID:g166979
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A;Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-392,
A;Cross-references: GB:J04202; NID:9166984; PIDN:AAA98615.1; PID:9166985
A;Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B
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A;Experimental source: gene Amy56 for alpha-amy1ase
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A; Residues: 1-429 < RAH>
                                                                                                                                   A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
                                                                                                                                                                                                            A; Introns: 29/3; 346/3
                                                                                                                                                                                                                                                                                     A;Gene: Amy1
                                                                                                                                                                                                                                                                                                                                                       A; Gene: Amy46
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                                                                                                                                                                                                                                                 A; Map position: 6
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ol. Biol. 9, 3-17, 1987
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53, 18953-18960, 1988
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A94535
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A;Experimental source: cv. Himalaya R;Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B. FEBS Lett. 363, 299-303, 1995
A;Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-A;Reference number: S65602; MUID:95255567; PMID:7737421
                                                                                                                                                                 R;Rogers, J.C.; Milliman, C.
R;Rogers, J.C.; Milliman, C.
J. Biol. Chem. 258, 8169-8174, 1983
J. Biol. Chem. 258, 8169-8174, 1983
A;Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
                                                                                                                                                                                                                                                                                                    alpha-amylase (EC 3.2.1.1) precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999
C;Accession: A00846; S65602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-31/Domain: signal sequence #status predicted <SIG>F;32-383/Product: alpha-amylase #status predicted <MATF;150-289/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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A;Title: Structural organization and differential expres A;Reference number: JT0945; MUID:91088278; PMID:2263460
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C;Date: 31-Dec-1992 #sequence_revision
C;Accession: S19142; PS0158
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A; Residues: 1-383 <KIM>
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                                                                                                               A;Molecule type: mRNA
A;Residues: 1-438 <ROG>
A;Cross_references: GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987
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A; Residues: 1-50 < HUA>
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8; Conserv
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88.9%;
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Pred. No.
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Pred. No. 0.036;
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R; Rogers, J.C.

J. Biol. Chem. 260, 3731-3738, 1985

A; R; Rogers, J.C.

A; R; Rogers, J.C.

A; R; Rogers, J.C.

A; Ritle: Two barley alpha-amylase gene families are regulated differently in aleurone of A; R; Rogers of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months of Months
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ALBHB
ALBHB
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-am
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change
C;Accession: A31960; A00847; JE0405; A20267; A24457; A30759
R;Khursheed, B.; Rogers, J.C.
J. Biol. Chem. 263, 1895-18960, 1988
J. Biol. Chem. 263, 1895-18960, 1988
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C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: calcium binding; glycosidase; hydrolase; monomer; po
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-438/Product: alpha-amylase *status predicted <MAT>
F;171-318/Domain: alpha-amylase core homology <AMY>
F;204,229,315/Active site: Asp, Glu, Asp #status experimental
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A:Molecule type: protein
A;Residues: 25-29 <UGS>
C;Comment: Production of this enzyme in barley is hormonally regulated. Germinat:
C;Function:
C;Function: Catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: Wheat alpha-amylase; alpha-amylase core homology
A; Molecule type: protein
A; Residues: 25-59,'X',61-67,'HX',70-85,
C; Comment: The mRNA of this isozyme (B)
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Similarity 80.0%;
8; Conservet
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    'X',87-92,'E',94;146-165;228-251;297-303,'X',305-
is present at very low levels in unstimulated all
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RESULT 5
S07040
S07040
alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley C; Species: Hordeum vulgare (barley)
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22 C; Accession: S07040
R; Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S. Plant Mol. Biol. 9, 3-17, 1987
A; Title: Structure and organization of two divergent alpha-amylase A; Reference number: S06275
A; Accession: S07040
A; Molecule type: DNA
A; Residues: 1-437 < KNO>
A; Residues: 1-437 < KNO>
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C;Genetics:

A;Gene Amy2-2

A;Map position: 6

A;Map position: 6

A;Introns: 29/3; 344/3

A;Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-C;Finction:

C;Finction:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: 9,1ycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosida
E;1-24/Domain: signal sequence #status predicted <SIG>
F;25-427/Product: alpha-amylase systemental <MAT>
F;170-316/Domain: alpha-amylase systemental <MAT>
F;170-316/Domain: alpha-amylase ore homology <AMY>
F;25/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone ca F;203,228,313/Active site: Asp, Glu, Asp #status predicted
RESULT 6
$12825

alpha-amylase (EC 3.2.1.1) 3D - rice
C.Species: Oryza sativa (rice)
C.Species: Oryza sativa (rice)
C.Species: Oryza sativa (rice)
C.Accession: $12625; $12776; $15054; JT0945
C.Accession: $12625; $12776; $15054; JT0945
R.;Huang, N.; Koizumi, N.; Reinl, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A.Title: Structural organization and differential expression of rice alpha-approximation number: JT0945; MUID:91088278; PMID:2263460
A;Accession: $12625
A;Molecule type: DNA
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A:Map position: 1

A:Introns: 29/3; 74/1; 345/3

C:Function:

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic 1,4-bellion: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic 1,4-bellion: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic 1,5-bellion: cyseymords: glycosidase; hydrolase; polysaccharide degradation cyseymords: glycosidase; hydrolase; polysaccharide degradation filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase core homology camy's filto-site alpha-amylase cor
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A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 VNWVDKVGG
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Pred. No. 1.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               divergent alpha-amylase
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A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;170-314/Domain: alpha-amylase core homology <AMY> F;203,228,311/Active site: Asp, Glu, Asp #status predicted
RESULT 8
S10013
alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-amylase (EC 3.2.1.1) isozyme I - rice
N;Alternate names: 1,4-gulcan glucanohydrolase I
C;Specias: Oryza sativa (rice)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7137; PC7039
                                                                                                                                                                                                                                                                                     A;Gene: amy-I
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: calcium binding; germination; glycosidase; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: JC7137; A; Accession: JC7137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Abe, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T. Blosci. Blotechnol. Blochem. 63, 1329-1335, 1999
A;Title: Characterization of chameric enzymes constructed between two distinct alpha-amy A;Reference number: JC7137; MUID:99430781; PMID:10500994
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A; Residues: 1-72,'R',75-136,'R',138-435 <ON2>
A; Cross-references: EMBL:M24287; NID:g169754; PIDN:AAA33886.1; PID:g169755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April A; Description: The alpha-amylase genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:M24287 R;O'Neil, S.D.; Kumaqai, M.H.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-435 <HUA>
A;Residues: 1-435 <HUA>
A;Cross-references: EMBL:M59351; NID:g169770; PIDN:AAA33895.1; PID:g169771
R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Ro
Mol. Gen. Genet. 221, 235-244, 1990
                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 245-252 <ABZ>
C;Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages is important in germinating seeds and is present as multiple isoforms.
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A; Residues: 1-435 < ABE>
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A; Residues: 1-435 <ONE>
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Matches 8
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                                                                                                                                                                                                        Similarity
8; Conserv
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8; Conserv
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    (EC
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88.9%;
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Pred. No. 2
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    (clone lambda-OSg2)
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C;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
C;Accession: S10013
R;Huang, N.; Sutliff, T.D.; Litts, J.C.; Rodriguez, R.L.
Plant Mol. Biol. 14, 655-668, 1990
                                                                                                                                         $14958
alpha-amylase (EC 3.2.1.1) - rice
c;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: $14958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homolog: C;Keywords: glycosidase; hydrolases; polysaccharide degradation F;176-323/Domain: alpha-amylase core homology <AMY> F;209,234,320/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R. Mol. Gen. Genet. 221, 235-244, 1990
A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and A;Reference number: S12775; MUID:90318322; PMID:2370848
A;Recession: S12775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-amylase (EC 3.2.1.1) precursor (clone pOS103) - C;Species: Oryza sativa (rice) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #tcC;Accession: S12775
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A; Residues: 1-428 < HUA>
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R;Sutliff, T.D.; Huang, N.; Litts, J.C.; Rodriguez, R.L. Plant Mol. Biol. 16, 579-591, 1991
A;Title: Characterization of an alpha-amylase multigene A;Reference number: S14956; MUID:91329692; PMID:1714318
A;Accession: S14958
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Pathway:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-434 <ONE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 30/3; 75/1; 345/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:M24286; NID:g169752; PIDN:AAA33885.1; PID:g169753
                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathway: glycogen/starch degradation;
Superfamily: wheat alpha-amylase; alpha-amylase core homology;
Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                     259
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNWVDRVGGA
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70.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
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                                                                               in
                                                                                                                                                                        22-Jun-1999
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cluster

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A, Molecule type: DNA
A, Residues: 1-440 <SUT>
A, Cross-references: EMBL:X56336; NID:g20334; PIDN:CAA39776.1; PID:g20335
A; Cross-references: EMBL:X56336; NID:g20334; PIDN:CAA39776.1; PID:g20335
C; Function:
A; Introns: 33/3; 78/1; 346/3
C; Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; pescription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C; Superfamily: wheat alpha-amylase; alpha-amylase core homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 174-318/Domain: alpha-amylase core homology <AMY>
F; 207, 232, 315/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fructose-permease IIBC component fruA homolog - Mycoplasma genitalium
C;Specles: Mycoplasma genitalium
C;Specles: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C;Accession: H64206
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Mguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.,
C.A.; Yenter, J.C.
                                                                                                                                                                                                                                                        hypothetical protein 27 - phage HP1
C;Species: phage HP1
C;Species: phage HP1
C;Date: 06-Dec-1968 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C;Accession: S69535
R;Esposito, D; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, P.
Nucleic Acids Res. 24, 2360-2368, 1996
A;Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Reference number: S69503; MUID:96279738; PMID:8710508
A;Rocession: S69535
A;Accession: S69535
A;Accession: S69536
A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-680 <TIGR> A;Cross-references: GB:U39685; GB:L43967; NID:g3844658; PIDN:AAC71279.1; PID:: A;Experimental source: strain G-37 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genetic code: SGC3
C;Superfamily: phosphotransferase system enzyme II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64206
                                                                                                                               A;Cross-references: EMBL:U24159; NID:g1046235; PIDN:AAB09214.1; PID:g1046256 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Apri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 6
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Best Local S
Matches 7
                                                                                                                                                                                                                                                               Status: preliminary; nucleic acid sequence not shown; translation not shown
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       Local Similarity 75.
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58 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 NWLNKLGG 353
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                                                                                                                                                                                                   <ESP>
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                                     73.2%;
   Score 41; DB:
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 2;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2; Length 440
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                   Length 689
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       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAC71279.1; PID:g1045736;
                                                                                                                                                                                                                                                                                                                                                                                                                         S.D.; Waldman, A.S.;
   0;
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   Gaps
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136856

B18L protein - variola virus

N;Alternate names: B17L protein (COP)

C;Species: variola virus

N;Alternate names: B17L spotein (COP)

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001

C;Accession: 136856; S46875

R;Bilinov, V.M.

R;Bilinov, V.M.

R;Bilinov, V.M.

A;Reference number: A36859

A;Accession: 13685

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-340 <BLI>
A;Residues: 1-340 <BLI>
A;Residues: 1-340 <BLI>
A;Residues: Strain India-1967, ssp. major, isolate Ind3

R;Kolykhalov, A.A.; B1nov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F.

A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H.

A;Reference number: S46868

A;Accession: $46868

A;Residues: 1-340 <KOL>
A;Residues: 1-340 <KOL>
A;Residues: SMBL:X67117; NID:g516428; PIDN:CAA47527.1; PID:g516436

A;Experimental source: strain India-1967, isolate Ind3

C;Superfamily: vaccinia virus probable 39.6K protein
                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein B15L - variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28614
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au |
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au |
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au |
R;Mature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir |
A;Accession: T28614
A;Accession: T28614
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RESULT 15
B72174
D7L protei
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Best Local S
Matches 7
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Best Local
   protein
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                                                                                                                                                                                                                                                                                         71.4%;
Similarity 77.8%;
7; Conservation
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                                                                                                                                                                     NWVSKVGDS
   variola minor virus
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77.88;
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                                                                                                                                                                                                                                                                                             1; Mismatches
   (strain Garcia-1966)
                                                                                                                                                                                                                                                                                                                           Score 40; DB 2;
Pred. No. 19;
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Pred. No. 19;
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RESULT 12 S69535

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probable 39.6K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A;Variety: strain Ankara
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Jun-2000
C;Accession: T37451
R;Antoine, G.; Scheifflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MV A;Reference number: 220877
A;Accession: T37451
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-340 <ANT>
A;Residues: 1-340 <ANT>
A;Cross-references: EMBL:U94848; PIDN:AAB96481.1
A;Experimental source: strain Ankara
C;Genetics:
A;Note: MVA185L
C;Superfamily: vaccinia virus probable 39.6K protein
                      RESULT 17
G42527
B17L protein - vaccinia virus (strain Cop. C; Species: vaccinia virus A; Note: host Homo sapiens (man) C; Date: 09-Nov-1990 #sequence_revision 09 C; Accession: G42527
R; Johnson, G.P.
submitted to GenBank, June 1990 A; Reference number: A33172 A; Accession: G42527 A; Accession: G42527 A; Accession: G42527 A; Residues: 1-340 <JOH>
C; Superfamily: vaccinia virus probable 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000
C;Accession: B72174
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, submitted to GenBank, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
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C;Superfamily:
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A;Experimental source: strain
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A; Residues: 1-340 <SHC>
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Best Local S
Matches 7
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Best Local S
Matches 7
Query Match
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                            virus probable 39.6K protein
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77.88;
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77.8%;
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Garcia-1966
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Score 40;
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19;
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19;
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Length 340;
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alpha-amylase (EC 3.2.1.1) - rice
C;Species: Oryza sativa (rice)
C;Date: 22-Nov-1993 #sequence_revision
                                           RESULT
S19990
                                                                                                                                                                                                                                                                                                                        A;Gene: RAmy2A
A;Introns: 27/3;
C;Function:
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JQ1527
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A; Residues: 1-340 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-443 <HUA>
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77.8%;
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60.08;
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 10-Nov-1995 #text_change 22-Jun-1999
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alpha-amylase (EC 3.2.1.1) 2A - rice
C;Species: Oryza sativa (rice)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change
C;Accession: JQ1527
R;Huang, N.; Reinl, S.J.; Rodriguez, R.L.
Gene 111, 223-228, 1992
A;Title: RAmy2A; a novel alpha-amylase-encoding gene in rice.
A;Reference number: JQ1527; MUID:92175526; PMID:1541400
A;Accession: JQ1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A:Title: Nucleotide sequence of 42kbp of vaccinia virus
A:Reference number: JQ1767; MUID:91259063; PMID:2045793
A:Accession: JQ1810
                                                                                   A;Pathway: glycogen/starch degradation C;Superfamily: wheat alpha-amylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;168-317/Domain: alpha-amylase core homology <AMY> F;202,228,314/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: JO1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: DDBJ:D11079; NID:g222717; PIDN:BAA01846.1; C;Superfamily: vaccinia virus probable 39.6K protein
                                                                                                                                                                                                   A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M74177; NID:g169768; PIDN:AAA33894.1; PID:g169769
C;Comment: Rice alpha-amylaseses are encoded by three multigene families,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccinia virus (strain WR)
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1; Mismatches
                   Score 40;
Pred. No.
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Pred. No.
  Mismatches
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RESULT 22
AG1312
thioredoxin homolog lmo1903 [imported] - Listeria monor thioredoxin homolog lmo1903 [imported] - Listeria monor C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #te
C;Accession: AG1312
C;Accession: AG1312
R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dus Dijones, L. M.; Karst, U.
D; Jones, L. M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, Xuhn, M.; Kunst, F.; Kurapkat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S19990
R;Goldman, S.; Mawal, Y.; Wu, R.
submitted to the EMBL Data Library, February 1992
A;Reference number: S19990
A;Recession: S19990
A;Rocession: MRNA
A;Residues: 1-445 <GOL>
A;Rolecule type: mRNA
A;Residues: 1-445 <GOL>
A;Cross-references: EMBL:X64619; NID:g20172; PIDN:CAA45903.1; PID:g20173
C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; olysaccharide degradation
F;168-317/Domain: alpha-amylase core homology <AMYP
F;202,228,314/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Genetics:
A;Gene: env
C:Superfamily: BIV env polyprotein
C:Superfamily: BIV env polyprotein; coat protein; glycoprotein; immunodeficiency; polyprot
C;Keywords: AIDS; capsid protein; coat proteid edd <SIG:
F;1-13/Domain: signal sequence #status predicted <GP1>
F;14-555/Product: coat protein gp62 #status predicted <GP2>
F;556-904/Product: coat protein gp40 #status predicted <GP2>
F;556-972/Domain: transmembrane #status predicted <TN1>
F;729-747/Domain: transmembrane #status predicted <TN3>
F;827-843/Domain: transmembrane #status predicted <TN3>
F;827-843/Domain: transmembrane #status predicted <TN3>
F;131,255,277,296,329,367,376,385,410,427,432,452,491,509,541,597,663,694,877/Binding si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     env polyprotein precursor - bovine immunodeficiency virus (isolate 127)

N;Alternate names: coat polyprotein
N;Contains: coat protein gp40; coat protein gp62

C;Species: bovine immunodeficiency virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-1997

C;Accession: E34742

R;Garvey, K.J: Oberste, M.S.; Elser, J.E.; Braun, M.J.; Gonda, M.A.

Virology 175, 391-409, 1990

A;Title: Nucleotide sequence and genome organization of biologically active proviruses
A;Reference number: A4742; MUID:90223985; PMID:2183467

A;Recession: E34742

A;Molecule type: genomic RNA
A;Residues: 1-904 <GARN
A;Residues: 1-904 <GARN
A;Residues: GB:M32690
C;Genetics:
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                               2 NWVNKVGGS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 71.4%;
Similarity 60.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                NWLNKIGES 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                        lmo1903 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 904; Pred. No. 50; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                      27-Nov-2001 #text_change
                           Kurapkat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 445
                                                                                                         A.; Baquero,
Dussurget, O.;
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                               G.;
                               Madueno,
                                                                                                      F.; Berche, P.; Entian, K.D.;
                                                                                                                                                                                      27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                           E.; Maitournam,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                   ; Bloecker
Fsihi, H.
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RESULT 23
AG1684

Athoredoxin homolog lin2017 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1684
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.,
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Tatile: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Ccession: AG1684
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 cG1A>
A;Cross-references: GB:AL592022; PIDN:CAC97247.1; PID:g16414518; GSPDB:GN00178
A;Gene: lin2017
RESULT 24
H72668
hypothetical protein APE0774 - Aeropyrum pernix (strain K1)
C;Boecies: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: H72668
R;Rawarabayasi, Y:; Hino, Y:; Horikawa, H.; Yamazaki, S.; Haikawa, Y:; Jin-no, K.; Talawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A;Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339; pMID:10382966
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: DNB0:APE00060; NID:95104188; PIDN:BAA79752.1; PID:d1043538; PID:g
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0774
C;Superfamily: Aeropyrum pernix hypothetical protein APE0774
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Best Local S
Matches 6
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6; Conserv
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6; Conser
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nilarity 75.0%;
Conservative
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Pred. No. 13;
1; Mismatches
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1231
RESULT 27
JE0408
3'-nucleotidase (EC 3.1.3.6) PA3
N;Alternate names: nuclease PA3
C;Species: Penicillium sp.
                                                                                                                                                                                                                                  A; Residues: \bar{1}^-270 <MAE> C; Superfamily: Penicillium citrinum nuclease
                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 200, 651-661, 1991
A;Title: Primary structure of nuclease Pl from Penicillium citrinum A:Reference number: S17828; MUID:92007841; PMID:1915339
A;Accession: S17828
                                                                                                                                                                                                                                                                                                                                                                              C;Species: Penicillium citrinum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jun-2000
C;Accession: S17828
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S17828
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C;Superfamily: alpha-glucosidase; alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:NC_003210; PIDN:CAC99332.1; A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha.alpha-phosphotrehalase homolog lmo1234 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Decies: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AF1231
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                                                                                                                                                                                                                                                                                                                                                                                                                               nuclease S1 -
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A; Residues: 1-548 <GLA>
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                                                                                                              밁
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Matches
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                                                                                                              NWINEIHGS
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55.68;
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55.6%;
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                                Penicillium
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46;
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A;Title: Nucleotide sequence of cDNA for alpha-amylase from A;Reference number: S10514; MUID:90332425; PMID:2377468 A;Accession: S10514

cotyledons of germinating

Nucleic Acids Res. 18, 4250, 1990

D.; Minamikawa,

R;Yamauchi,

A;Molecule type: protein A;Residues: 24-31 <YAW> R;Takeuchi, H.; Yamauchi, D.; Wada, S.; Minamikawa,

A; Description: Nucleotide

sequence of the alpha-amylase gene

from Vigna mungo

June 1993

Ξ.

submitted to the EMBL Data Library,

A;Cross-references: EMBL:X53049; NID:g22059; A;Accession: S61336

PIDN:CAA37217.1;

PID: g22060

A; Molecule type: mRNA A; Residues: 1-421 <YAM> alpha-amylase (EC 3.2.1.1) precursor - black gram (;Species: Vigna mungo (black gram) C;Species: Vigna mungo (black gram) C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999 C;Accession: S10514; S61336; S40201; S61334

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C; Date:
C; Access
                                                                                                                                                                                                                                       th, T.; Connercu, A.; Alara, P.; S.; Moule, S.; O'Gaora, P.; S.; Moule, S.; O'Gaora, P.; Nature 413, 848-852, 2001

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s.
                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: Penicillium citrinum nuclease S1
C;Keywords: glycoprotein; phosphoric monoester hydrolase; zinc
F;92,138,184,197/Binding site: carbohydrate (Asn) (covalent) #status
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A;Title: Primary structure of a nuclease (nuclease PA3)
A;Reference number: JE0408; MUID:91299282; PMID:1369324
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A; Residues: 1-278 < PAR>
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A;Residues: $1-421 < fnAk
A;Residues: $1-421 < fnAk
A;Residues: $1-421 < fnAk
A;Cross-references: EMBL:X73301; NID:g437944; PIDN:CAA51734.1; PID:g437945
C;Genetics:
A;Introns: $28/3; 72/1; 340/3
C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
E;1-23/Domain: slyna-amylase status predicted <510>
F;24-42/Product: alpha-amylase #status predicted <4MT>
F;168-312/Domain: alpha-amylase core homology <AMY>
F;201,226,309/Active site: Asp, Glu, Asp #status predicted
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c.Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. FCC 7120
A:Note: Nostoc sp. Strain PCC 7120
c:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
c:Accession: AD2161
R:Kaneko T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2161
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-627 -KURD
A:Cross-references: GB:BA000019; PIDN:BAB74542.1; PID:g17131937; GSPDB:GN00179
A:Experimental source: strain PCC 7120
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FFRS_CALMOUSE
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Query Match
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Matches 10
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01-NOV-1990 (Rel. 16, Last sequence upon 15-DEC-1998 (Rel. 37, Last annotation upon Alpha-amylase type B isozyme precursor glucan glucanohydrolase)
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AMY6_HORVU
P04750;
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                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahmatullah R.J., Huang J.-K
Chandra G.R., Muthukrishnan
                                                                                                                                                                   EMBL; X15227; CAA33299.1; -. EMBL; K02636; AAA32932.1; -. PIR; JE0406; JE0406. HSSP; P04063; 1AVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
MEDLLNE-8315940; PubMed-6335720;
Huang J.-K. Swegle M., Dandekar A.M., Muthukrishnan S.;
"Expression and regulation of alpha-amylase gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                           SEQUENCE
                                                                             CHAIN
                                                                                          SIGNAL
                                                                                                                        Pfam; PF00128; alpha-amylase; SMART; SM00642; Aamy; 1.
                                                                                                                                             InterPro; IPR006589; Alp_amyl_cat_sub
InterPro; IPR006047; Alpha_amyl_cat.
                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMY 1.6
                                                                                                    Calcium;
                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION
                                                                                                                                                                                                                                                                                                                 KNOWN
                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY
                                                                                                                                                                                                                                                                                                                                      GIBBERELLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                        BARLEY
                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
           Similarity
                                                                                                    Multigene
                                                                                                                                                                                                                                                                                                                AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum
                                                                                                               Glycosidase; Carbohydrate metabolism;
                                          205
315
429 /
100.0%; ilarity 100.0%; Conservative
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Huang J.-K., Clark K.L.,
                                                                 429
205
                                                                                                   family;
                                           47937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Clones GRAMY56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptophyta; Embryophyta; Tracheophyta;
/ta; Liliopsida; Poales; Poaceae; Pooideae;
                                              W.
                                                                                                   Signal.
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:
                                                        BY
YB
                                                                             ALPHA-AMYLASE
 Score 56; DB 1; Pred. No. 0.014; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                           1C924CA6319D5262
                                                       SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                             13
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r (EC 3.2.1.1) (1,4-alpha-D-
Y56 and 963).
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(See http://www.isb-sib.
                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                                          GLYCOSYL HYDROLASES,
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                                                                              TYPE
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                     Length 429
                                                                                                               Seed; Germination;
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RESULT 2
AMC1_ORYSA
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-amylase isozyme C precursor (EC 3.2.1.1)
                                                CHAIN
SEQUENCE
                                                                                      Hydrolase;
Multigene :
                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucanohydrolase) (Isozyme AMYC OR AMY1B.
                                                                                                                           PIR; S19142; ALRZOC.
HSSP; P04063; 1AVA.
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amylase genes.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91088278; PubMed=2263460; Huang N., Koizumi N., Reinl S., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence Plant Mol. Biol. 18:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim J.-K., Wu R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92119260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                 Gramene;
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                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural organization
                                                                           SIGNAL
                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO BE
FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERMINATION.
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                                                                                                                                                    X52240; CAA36485.1;
M59350; AAA33893.1;
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Similarity
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                                                                                                                 P27940;
                                                                                      family.
                                                  383
                                                                                                     Glycosidase;
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 Conservative
                                                  ΑĄ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ence of a high-pI rice
18:399-402(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -IR26; TISSUE-Leaf; PubMed=1731997;
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383
43254
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             87.5%;
88.9%;
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  ۲.
             Score 49;
Pred. No.
                                               POTENTIAL.
ALPHA-AMYLASE ISOZYME C.
7426BF8E7C411B54 CRC64;
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  Mismatches
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                                                                                                     metabolism;
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              DB 1
0.22;
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a; Poales; Poaceae;
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Matches 8
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PIR, A00846; ALBH
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR06047; Alpha_amyl_cat.
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J. Biol. Chem. :
-!- CATALYTIC A(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00128; alpha-amylase;
SMART; SM00642; Aamy; 1.
Hydrolase; Glycosidase; Carbol
Calcium; Multigene family; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMYI) (Low pI alpha-amylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cv. Himalaya;
MEDLINE-83238423; Publ
Rogers J.C., Milliman
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CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic caralytic activity: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

SUBCELLULAR LOCATION: Extracellular:

SUBCELLULAR LOCATION: Extracellular:

DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-ANYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACLD, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-ANYLASE. THE ENZYME THEN DEGRADES THE STARCH MITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STWILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
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1 VNWVNKVGGS
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5 VNWVNRVGG 234
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Pred. No. 0.38
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13-AUG-1987 (Rel. 05, Last
15-JUL-1999 (Rel. 38, Last
Alpha-amylase type B isozy
glucan glucanohydrolase) (
AMY1.3.
                                                                                                                                        Hydrolase; Glycosidase; Carb
Calcium; Multigene family; S
SIGNAL 1 24
CCHALN 25 >368
ACT_SITE 203 203
ACT_SITE 208 228
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ACT_SITE 313 313
NON_TER 368 368
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                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable tween the Swiss Institute of Bioinformatics and the EMBL outsy the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
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P04747;
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Eukaryota; Viridiplantae;
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InterPro; IPR006047;
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                                                                                                                                                                                                                                                                                                       InterPro;
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MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.

MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.

CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nt Mol. Biol. 3:407-418(1984).

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

DEVELOPMENTAL STACE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH MITHIN 10 HOURS STIMULATES THE ALEURONE GELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
                                                              Similarity
8; Conser
                            VNWVNKVGG
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368
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05, Last sequence update)
38, Last annotation update)
88 B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-colase) (Clone PHV19) (Fragment).
                                                                                                                             40787
                                                                           83.9%;
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Alpha_amyl_cat.
-amylase; 1.
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0
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on alpha-amylase
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RESULT
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                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W., Svensson B., Haser R.;
"Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9-A resolution.";
Structure 6:649-659(1998).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMY2_HORVU STANDARD; PRT; 427 AA. P04063; P04063; 01-NOV-1986 (Rel. 03, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-SBP-2003 (Rel. 42, Last annotation update) 15-SBP-2003 (Rel. 42, Last annotation update) Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase)
                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=94254083; Pubmed=6196040;
Kadziola A., Abe J.-I., Svensson B., Haser R.;
"Crystal and molecular structure of barley alpha-amylase.";
J., Mol. Biol. 239:104-121(1994).
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"Two barley alpha-amylase gene families
aleurone cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rahmatullah R.J., Huang J.K., Clark K.L., Reeck Chandra G.R., Muthukrishnan S.;
"Nucleotide and predicted amino acid sequences for high-pl alpha-amylases from barley.";
Plant Mol. Biol. 12:119-121(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
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                                                                                                                                                                                                                  11nkages in oligosaccharides and polysaccharides.
COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
                                                                                                                                                            GIBBERELLIC ACI
                                                                                                                           KNOWN AS
                                                                                                                                      SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                             DEVELOPING PLANT EMBRYO. INDUCTION: TYPE B ISOZYME MRNA IS
                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
 X15226;
K02637;
                                                                                                                                                                                 TION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
                                                                                                                           THE ALPHA-AMYLASE FAMILY.
CAA33298.1; -. AAA98790.1; -.
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                                                                                                                                                                                                                                                                                                                                                                    PubMed=9634702;
                                                                                                                                                            THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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1BG9; 15-JUN-99.
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1AMY; 13-MAY-95.
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IGF -> Q
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RY MEDLING-90318322; PubMed-2370848;

RA MCDLING-90318322; PubMed-2370848;

RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,

RA ROdriguez R.L.;

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01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan AMY1 3 OR AMY3D.
                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. Japonica M202; TISSUB-Ettolated leaf; MEDLINE-91088278; PubMed-2263460; Huang N., Kolzumi N., Reinl S., Rodriguez R.L.; "Structural organization and differential expression amylase genes."; uncleic Acids Res. 18:7007-7014(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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EMBL; M24287; AAA3386.1; -
PIR; S12625; S12625.
HSSP; P04063; 1AVA.
Gramene; P27933; -
InterPro; IPR006589; Alp_am;
InterPro; IR0006047; Alpha_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMY1_ORYSA STANDARD; PRT; 428 AA.
P17654;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).
AMY1. OR AMY1.
SEQUENCE FROM N.A. (CLONE POS103).

STRAIN=CV. Japonica M202;
MEDLINE=90318322; pubMed=2370848;
O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff
Rodriguez R.L.;
"The alpha-amylase genes in Oryza sativa: characterization
"The alpha-amylase genes in Oryza sativa: characterization
clones and mRNA expression during seed germination.";
MOI. Gen. Genet. 221:235-244(1990).

-i- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH E
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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InterPro; IPRO06047; Alpha_amyl_c
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
Hydrolase; Glycosidase; Carbohyd
                                                                                                                                                                                                                                                                               STRAIN=cv. Japonica M202;
MEDLINE-91146657; PubMed-2102847;
Huang N., Sutliff T.D., Litts J.C., F
"Classification and characterization
multigene family.";
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253 VNWVNAVGG
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Mol. Biol. 14:655-668(1990).
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alp_amyl_cat_sub.
Alpha_amyl_cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carbohydrate metabolism; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

ALPHA ANYLASE ISOZYME 3D.

ALPHA ANYLASE ISOZYME 3D.

BY SIMILARITY.

BY SIMILARITY.

CALCIUM (BY SIMILARITY).

CALCIUM (BY SIMILARITY).

CALCIUM (BY SIMILARITY).

PO -> R (IN REF. 2).

P -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1;
Pred. No. 0.85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1BBD6AB195BA0D6E CRC64;
                                                                                                                                                                                                                                                                                                       Rodriguez R.L.;
n of the rice alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embryophyta; Tracheophyta; ; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                          Sutliff T.D.,
     DURING
                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 8
AM3A,O
AM3A,O
AC P27932
DT 01-AUG
DT 01-AUG
DT 15-SEP
DE Alpha-
DE 9lucan
GN AMY1.2
OS OTYZA
OC Eukary
OC Ehrhar
OC Ehrhar
OC Ehrhar
OC Sperma
OC Sperma
OC SPERMA
OC STRAIN
RX MEDLIN
RA SULLIÍT
                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M24286;
PIR; S10013; S
HSSP; P04063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PRO7 entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  Eukaryota; Viridipiantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + +
                                                                                                                                            glucan glucanohydrolase).
AMY1.2 OR AMY3A.
                                                                                                                                                                       01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Alpha-amylase isozyme 3A precursor (EC 3.2.
                                                                                                                                                                                        P27932;
01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006589; Alp_amyl_cat_sub
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
 STRAIN-cv. Japonica M202; TISSUE-Etiolated leaf; MEDLINE-91329692; PubMed-1714318; Sutliff T.D., Huang N., Litts J.C., Rodriguez R.
                                                                                                                               Oryza sativa (Rice).
                                                                                                                                                                                                                                                  AM3A_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0110; ALPHI SMART; SM00642; Aamy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gramene; P17654;
                                              SEQUENCE
                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
SUBUNIT: MONOMER.
TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL. PTM: ONLY CEREAL ANYLASE KNOWN TO BE GLYCOSYLATED. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALLUS, YOUNG ROOTS AND LEAVES.

DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERMINATION CATALYTIC AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S10013; S10013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X16509; CAA34516.1;
M24286; AAA33885.1;
                                                                                                                                                                                                                                                                                                                       253 VNWVDRVGGA
                                                                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                           FROM
                                                                                                                                                                                                                                                                                                                                                   VNWVNKVGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                    26
203
314
116
174
265
428 /
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHAAMYLASE.
                                                                                                                                                                                                       23, Created)
23, Last sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
428
203
314
116
174
265
                                                                                                                                                                                                                                                                                                                       262
                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                      47755 MW;
                                                                                                                                                                                                                                                                                                                                                                                            80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carbohydrate metabolism; Calcium; Signal;
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-AMYLASE.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (GLYMAC. . .) (PRO
N-LINKED (GLCNAC. . .) (PRO
N-10 3B71403AACFFC6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Score 45; |
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                          (EC 3.2.1.1)
  Rodriguez R.L.
                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                                                                                                                                                       DB
1.3;
                                                                                                                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                 ₿
                                                                                                     Poales;
                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 428
                                                                                                                                                                          (1,4-alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DURING
E PLANT
                                                                                                     Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERMINATION HORMONE
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                       PTFA_MYCGE
                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PTS system, fructose-specific IIABC component
permease IIABC component) (Phosphotransferase
component) (EC 2.7.1.69) (EII-Fru/EIII-Fru).
FRUA OR MG062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TIS
-i- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERNINAN
IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
GIBBEREILIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL
-i- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006589; Alp_amyl_cat_sub
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X56336; CAA39776.1; -. PIR; S14958; S14958. HSSP; P04063; IAVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERMINATION.
-!- CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of an alpha-amylase multigene Plant Mol. Biol. 16:579-591(1991).
                                                                                                               Mycoplasma genitalium. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gramene; P27932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
                                                                                                                                                                                                                                                        PTFA_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family.
                                                                                                 NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                               257 VNWVKQVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00128; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                               1 VNWVNKVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00642; Aamy;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                             440
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHAAMY LASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
440
207
315
119
178
                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gosaccharides and polysaccharides
A CALCIUM ION REQUIRED FOR ITS A
                                                                                                                                                                                                                                                                                                                                                                                                                                            48872
                                                                                                                                                                                                                                                                                                                                                                                                 75.0%;
77.8%;
                                                                                                               Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carbohydrate metabolism; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMICALCIUM (BY SIMICALCIUM)
                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-AMYLASE ISOZYME
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALCIUM (BY SIMILARITY).
ALCIUM (BY SIMILARITY).
5E9B78C29AA91C2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  42;
No.
                                                                                                                                                                                                                                                           089
                                                                                                                                                                                                                                                                                                                                                                                                  DB
4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                 (EIIABC-Fru) (Fructose-enzyme II, ABC
                                                                                                                                                                                                                                                                                                                                                                                                                Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cluster in rice.";
                   Kelley J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERMINATION
HORMONE
                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration -
L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                x
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0

Fuhrmann

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InterPro; IPR002178; PTS_EIIA_2.
InterPro; IPR003352; PTS_EIIC.
InterPro; IPR003353; PTS_IIB_fruc.
InterPro; IPR003353; PTS_IIB_fruc.
InterPro; IPR004715; PTSIIA_fruc.
InterPro; IPR004715; PTSIIA_fruc.
Pfam; PP00359; PTS_EIIA_2; 1.
Pfam; PP02379; PTS_IIB_fruc; 1.
Pfam; PP02379; PTS_IIB_fruc; 1.
Pr0Dom; PD001689; PTS_EIIA_2; 1.
TIGRPAMS; TIGR00849; FTU; II.
TIGRPAMS; TIGR00849; FTU; II.
TIGRPAMS; TIGR00849; FTS_IIC_fructo;
TIGRPAMS; TIGR014477; PTS_IIC_fructo;
TIGRPAMS; TIGR01447; PTS_IIC_fructo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genitalium";
genitalium";
genitalium";
Genomics 1:151-164(1996),
Microb Comp. Genomics 1:151-164(1996),
Microb Comp. Genomics 1:151-180(1996),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U39685;
EMBL; U02138;
PIR; H64206; H
TIGR; MG062;
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 147-253 FROM N.A. STRALNE-AVGC 33530 / G-37, MEDLINE-94075230; PubMed-8253680; MEDLINE-94075230; PubMed-8253680; Hut Peterson S.N., Hu P.-C., Bott K.F., Hut "A survey of the Mycoplasma genitalium sequencing.", 1, Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISCUSSION OF SEQUENCE.
MEDLINE=98353635; PubMe
Reizer J., Paulsen I.T.
                                                                                                                                                                      MOD
                                                                                                                                                                                                                                         Phosphorylation;
DOMAIN 1
DOMAIN ?
                                                                                                                                                                                                                                                                                                             Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-98353655; PubMed-9689210;
Reizer J., Paulsen I.T., Reizer A., Titgemeyer F., Saier M.H
"Novel phosphotransferase system genes revealed by bacterial
analysis: the complete complement of pts genes in Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE SUGAR.

CATALYTIC ACTIVITY: Protein N-phosphohistidine + histidine + sugar phosphate.

SUBCELLULAR LOCATION: Integral membrane protein (
SIMILARITY: Contains 1 PTS EIIA domain.

SIMILARITY: Contains 1 PTS EIIG domain.

SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                      RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : н64206.
174
174
306
352
352
377
410
449
488
532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC71279.1; -.
AAD12415.1; -.
                                                                                                                                                                                 448; Irun, 1.48; PTS_IIC_fructo; 1.427; PTS_IIC_fructo; 1.525; PTS_IIC_fructo; 1.525; PTS_IIC_fructo; 1.525; PTS_IIC_fructo; 1.525; PTS_IIC_fructo; 1.525; PTS_IIC_BOMAIN.
680 EILB_DOMAIN.
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Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 296:2376-2379(2002).

Science 296:2376-2379(2002).
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P46240;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Shikimate 5-dehydrogenase (EC 1.1.1.25);
AROE OR BUSG474.
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Protebbacteria; Gammaproteobacteria; Enterobacteriales;
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"Characterization of a putative
aphidicola (endosymbiont of aphi
gene.";
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MEDLINE-95212914; PubMed-7535281;
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[2]
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                                                                                       virus (strain Copenhagen).
dsDNA viruses, no RNA stage;
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385 405 POTENTIAL.
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Pred. No. 10;
1; Mismatches
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                                                                                              Poxviridae;
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Matches
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VB17_1
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Protein B17.
B17L OR B16L.
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                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Appendix to 'The complete Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goebel S.J., Johnson G.P.,
Paoletti E.;
"The complete DNA sequence
Virology 179:247-266(1990).
                                                        EMBL; D11079
PIR; JQ1810;
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                              Orthopoxvirus
                                                                                                                                                                                                                                                                                     Vaccinia virus (strain
Viruses; dsDNA viruses,
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                                              SEQUENCE
                                                                                                                                                                                    J. Gen.
                                                                                                                                                                                                the
                                                                                                                                                                                                           Smith G.L., Chan Y.S., Howard S.T.; "Nucleotide sequence of 42 kbp of vaccinia virus
                                                                                                                                                                                                                                 MEDLINE=91259063; PubMed=2045793;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID=10254;
                                                                                                                                                                                               right inverted terminal repeat.";
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                                                                   D11079; BAA01846.1;
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Similarity 7; Conserv
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Pred. No. 7.9
l; Mismatches
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Pred. No. 7
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                                                                                                                                                                                                                                                                                          stage; Poxviridae;
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Query Match
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STRAIN-India-1967 / Isolate Ind3;

STRAIN-India-1967 / Isolate Ind3;

MEDLINE-92209372; PubMed=1666548;

Shchelkunov S.N., Marennikova S.S., Totmenin A.V., Blinov V.M.,

Chizhikov V.E., Gutcrov V.V., Safronov P.F., Pozdnyakov S.G.,

Chizhikov V.E., Gutcrov P.V., Anjaparidze O.G., Sandakhchiev L.S.;

Shelukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakhchiev L.S.;

"Creation of a clone library of fragments from the natural variola

virus and study of the structural and functional organization of

virus and study of the structural and functional organization of

virus and study of the structural and functional organization of

virus and study of the structural and functional organization of

viral genes from a circle of hosts.";

Dokl. Akad. Nauk SSSR 321:402-406(1991).
                                                                                                                                                                       EMBL;
                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-Somalia-1977, and Garcia-1966;

MASSUNG R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,

Totmenin A.V., Shchelkunov S.N., Esposito J.J.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bangladesh-1975;
MEDLINE-94088747; PubMed-8264798;
MEDLINE-94088747; PubMed-8264798;
MASSUNG R.F., Esposito J.J., Liu, L., Qi J., Utterback T.R.,
MASSUNG R.F., Esposito J.J., Liu, Parsons J.M., Loparev V.N.,
Knight J.C., Aubin L., Vuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-India-1967 / Isolate Ind3;
MEDLINE-93202281; PubMed-8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994
01-FEB-1994
01-FEB-1996
                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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P33878;
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B17L OR B18L OR B15L.
Variola virus.
                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter C.J.;
"Potential virulence determinants in terminal regions of variola smallpox virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
                                               LL; X69198; CAAA9127.1; -.
3L; X67117; CAAA7527.1; -.
3L; X72086; CAA50968.1; -.
3L; L12579; AAA60924.1; -.
3L; U18339; AAA63927.1; -.
3L; U18341; AAA69457.1; -.
3L; U18341; BA2174.
3; B72174; B72174.
3; 136856; 136856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ox virus genome.";
366:748-751(1993).
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annotation update;
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                                   C40C18C9CE692448 CRC64;
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DB 1; Length 340;
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01-AUG-1992
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M74177; AAA33894.1; -. PIR; JQ1527; JQ1527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linkages in oligosaccharides and polysaccharides.

- COPACTON: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

- SUBUNIT: MONOME:

- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.

- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. Japonica M202;
STRAIN-EV. Japonica M202;
MEDLINE-92175526; bubmed-1541400;
MEDLINE-92175526; bubmed-1541400;
"Ruang N., Rein1 S.J., Rodriguez R.L.;
"Ramy2A; a novel alpha amy1ase-encoding gene in rice.";
Gene 111:223-228(1992).
Gene 111:223-228(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza gativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORYSA
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                      Hydrolase;
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GERMINATION.
-i- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
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P27935;
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00128; alpha
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        1 VNWVNKVGGS
                                                       Similarity
6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                           IPR006047;
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2 (Rel. 23, Last sequ
3 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                         Glycosidase;
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60.0%;
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-amylase; 1.
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e 2A precursor (EC
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ALPHA AMYLASE ISOZYME 2A.
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1; Mismatches
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a; Poales; Poaceae;
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AMC2_ORYSA
ENV_BIV06
P19556;
O1-FEB-1991
O1-FEB-1991
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SEQUENCE
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Ol-AUG-1992 (Rel. 23, Created)
Ol-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase isozyme C2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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Gukaryota; Viridiplantae; Stre
Epermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
Multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldman S., Mawal Y., Wu R.;
Submitted (FEB-1992) to the
-!- FUNCTION: IMPORTANT FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gramene; P27941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING IN THE ALEUKONES CELLS UNDER THE CONTROL OF THE PLANT GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASE KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linkages in oligosaccharic COFACTOR: BINDS A CALCIUM
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S19990; S19990.
; P04063; IAVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC
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sen the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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yta; Liliopsida;
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ENV_BIV27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-90223985; PubMed=2183467;

Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.

"Nucleotide sequence and genome organization of biologically proviruses of the bovine immunodeficiency-like virus.";
                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                    CONFLICT
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Virology 175:391-409(1990).
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M74711; AAA42762.1; -.
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                                      Similarity 66. 6; Conservative
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66.78;
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(Coat polyprotein) [Contains: Coat protein
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Retroviridae; Lentivirus
                                      Score 40; DB Pred. No. 19; 2; Mismatches
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P19557; 01-FEB-1991 01-FEB-1991 16-OCT-2001 ENV polyprot

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MEDLINE-90223985; PubMed=2183467;
Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;

"Nucleotide sequence and genome organization of biologically active proviruses of the bovine immunodeficiency-like virus.";

Virology 175:391-409(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M32690; AAA91274.1; -. PIR; E34742; VCLJBT. HIV; M32690; ENV$BIV127.
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polyprotein precursor (Coa
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(Rel. 21, Last sequence update)
(Rel. 42, Last annotation update)
(EC 3.1.30.1) (Endonuclease P1) (Deoxyribonuclease
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MEDLINE-98393014; Pubmed-9726413;
Romier C., Dominguez R., Lahm A., Dahl O., Suck D.;
Recognition of single-stranded DNA by nuclease P1: hig
"Recognition of single-stranded DNA by nuclease P1: hig
crystal structures of complexes with substrate analogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.8 ANGSTEO MEDLINE-91266887; Pubbmed-1710977; Volbeda A., Lahm A., Sakiyama F., "Crystal structure of Penicillium resolution"; pmBO J. 10:1607-1618(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maekewa K., Tsunasawa
"Primary structure of
Tur. J. Biochem. 200:
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

NGPI_TaxID=5077;
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nasawa S., Dibo G., S
ure of nuclease P1 fr
. 200:651-661(1991).
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PubMed=1710977;
A., Sakiyama F., Suck
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rom Penicillium
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DT 01-MAR-1992
DT 15-5EP-2003
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Agric. Biol.
[2]
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01-MAR-1992 (Rel. 21, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Nuclease PA3 (EC 3.1.3.6) (Endonucleas
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Eurotiales; Trichocomaceae;
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01-MAR-1992
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Tabata N., Kazama
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                                                                                    Pfam;
                                                                                                    interPro;
                                                                                                                                               + phosphate.
COFACTOR: BINDS 3 ZINC IONS.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: TO A.ORYZAE NUCLEASE
                                                                                                                                                                                                                    FUNCTION: Hydrolyzes only single stranded apparent specificity for bases.
CATALYTIC ACTIVITY: A 3'-ribonucleotide +
                                                                                                                   JE0408; JE0408.
; P24289; 1AK0.
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                                                                                    PF02265; Nuclease;
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 ; Nuclease; Endonucle
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80 85 E
92 92 138 138 N
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a H., Ohgi K., Iri
re of a nuclease (
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t annotation update)
(Endonuclease PA3)
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clease; Glycoprotein; i
BY SIMILARITY.
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SPECIES-S.typhi; STRAIN-TY2 / ATCC 700931;
SPECIES-S.typhi; STRAIN-TY2 / ATCC 700931;
MEDLINE-22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayh
Burland V., Kodoyianni V., Schwartz D.C.,
""~~~~~rative genomics of Salmonella enter"
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CARBOHYD
                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wa Churcher C., Mungall K.L., BentLey S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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_SALTY
                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lat Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulv Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9L6T4; Q8Z336;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transcriptional regulator hdfr (H-NS-depdendent flhDC
HDFR OR STM3897 OR STMD1.99 OR STY3708 OR T3449.
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MEDLINE=21534947;
J. Bacteriol.
                      "Comparative and CT18.";
                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi
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185:2330-2337(2003). 
Negatively regulates
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R EMBL; AF233324; AAF33488.1; ALT_INIT.

R EMBL; AF233324; AAF33488.1; ALT_INIT.

R EMBL; AE016845; AAO70970.1; -.

R EMBL; AE016845; AAO70970.1; -.

R StyGene; SC7727; hdfR.

InterPro; IPR000847; HTH_Lysr.

R InterPro; IPR000847; HTH_Lysr.

R InterPro; IPR00126; Lysr_subst.

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01-AUG-1990
15-SEP-2003
                 SEQUENCE FROM N.A.

MEDILINE-9412001; PubMed-8290640;

MEDILINE-9412001; PubMed-8290640;

Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;

Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;

Tukeuchi H., Yamauchi D., Wada S., Minamikawa T.;

Tukeuchi H., Yamauchi D., Wada S., Minamikawa T.;

Plant Physiol. 103:1459-1459(1993)

- CATALTTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

- In CopacTors. BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, AI KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Cotyledon;
MEDLINE-9032425; PubMed-2377468;
MEDLINE-90332425; PubMed T.;
Yamauchi D., Minamikawa T.;
Nucleotide sequence of cDNA for alpha-amylase
germinating Vigna mungo seeds.";
Quileic Acids Res. 18:4250-4250(1990).
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01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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p50546; 1996 (Rel. 34, Created 01-OCT-1996 (Rel. 39, Last set 28-FEB-203 (Rel. 41, Last an DNA-directed RNA polymerase b
SEQUENCE OF 346-713 FROM N.A.
STRAIN-cv. Landsberg erecta; TISSUE-Cotyledon;
Knut J., Pfannschmidt T., Liere K., Link G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 23
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PRINTS;
SMART; S
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                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-20039611; PubMed-10574454;
MEDLS S. Nakamura Y., Kaneko T., Asamiz
"Complete structure of the chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CV. Landsberg erecta; TISSUE-Leaf;
MEDLINE-20069369; PubMed-10601874;
Pfannschmidt T., Ogrzewalla K., Baginsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPOB OR ATCG00190.
Arabidopsis thaliana (Mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53049; CAA37217.1; -.
EMBL; X73301; CAA51734.1; -.
FIR; S10514; S10514; S10514
HSSP; P04063; 1AVA.
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                                                                                                                                                                                                                                                                                                L.). Integration of a prokaryotic organelle-specific functions.";
J. Biochem. 267:253-261(2000).
                                                                                                                                                                                                                                                                                                                                             multisubunit chloroplast RNA polymerase A from mustard (Sinapis L.). Integration of a prokaryotic core into a larger complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPRO; IPRO06589; Alp_amyl_cat_sub.
PPRO; IPRO06047; Alpha_amyl_cat.
PPRO; IPRO06046; Glyco_hydro_13.
PP00128; Alpha-amylase; 1.
PP00128; Alpha-amylase; 1.
SM00642: Aamy; 1.
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(Rel. 39, Last sequence up
(Rel. 41, Last annotation
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1; Mismatches
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e of Arabidopsis
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PIR; S52324; S52324.

HSSP; QSKW07; IHQM.

InterPro; IPR001572; RNA_pol_B.

InterPro; IPR001572; RNA_pol_B.

Pfam; PF04563; RNA_pol_Rpb2_1; 1.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_6; 2.

Pfam; PF04560; RNA_POl_Rpb2_7; 1.

PROSITE; PS01166; RNA_POL_BETA; 1.
                               STRAIN-cv. Albatros; TISSUE-Cotyledon; MEDLINE-20069369; PubMed-10601874; Pfannschmidt T., Ogrzewalla v Tink G.;
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CONFLICT 2
CONFLICT 3
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alba
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                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; cc eurosids II; Brassicales; Brassicaceae; Sinapis. NCBI_TaxID=3728;
                                                                                                                                                                                                                                                                                                                                                                            P46818; Q9THV7;
01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINAL
RPOB_SINAL
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EMBL; AP000423; BAA84377.1; -.
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                               Chloroplast.
                                                                                                                                                                                                                                                                                                          Sinapis alba
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SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Belongs to the RNA polymerase beta chain family.
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CATALYTIC ACTIVITY: N nucleoside triphosphate =
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341 341 G
346 346 Y
599 599 L
927 927 T
958 959 VI
1038 1038 Q
1072 AA; 121049 MW;
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I -> V (IN REF. 2).
G -> S (IN REF. 2).
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L -> F (IN REF. 2).
T -> S (IN REF. 2).
VI -> DK (IN REF. 2).
VI -> DK (IN REF. 2).
Q -> P (IN REF. 2).
  prokaryotic
                                                                   K., Baginsky S.,
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                   RNA polymerase A from mustard
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chain (EC 2.
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                                                                 Sickmann A.,
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Best Local
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HSSP; Q9KWU7; 1HQM.

InterPro; IPRO01572; RNA_pol_B.

Pfam; PP04563; RNA_pol_Rpb2_1; 1.

Pfam; PP04561; RNA_pol_Rpb2_2; 1.

Pfam; PP04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

PROSITE; PS01166; RNA_POL_BETA; 1.
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01-AUG-1988
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Eur. J. Biochem. 267:253-261(2000).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; DNA-directed RNA polymerase; Transcription; Chloroplast.
CONFLICT 4 A -> S (IN REF. 1; CAA57814).
SEQUENCE 1078 AA; 121653 MW: BOCOF2367526DRF8 CEC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                 MEDLINE-88217525; PubMed-3368320;
Benatti L., Lorenzetti R., Dani M., Martini D., Sasano M., Sidoli A., Soria M.;
"A DNA sequence from Saponaria officinalis is si polymerase genes.";
Nucleic Acids Res. 16:3103-3103(1988).
                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales: Carvonhullancore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: In chloroplasts, the
                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast.
Eukaryota; Viridiplantae;
                           ÷
                                                                                                                                                                                                                                                                     TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saponaria officinalis (Common soapwort)
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3572;
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                 FUNCTION: DNA-DEPENDENT RNA POLIMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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(Rel. 08, Last sequence update)
(Rel. 41, Last annotation updat
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0; Mismatches
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RESULT 26
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ID R114_S
AC P78956
AC P78956
DT 01-NOV
DT 01-NOV
DT 30-MAY
DE Meiotit
GN REC114
OS Saccha
OC Eukary
OC Saccha
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01-NOV-1997 (Rel. 3:
01-NOV-1997 (Rel. 3:
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-DBVPG 6466 / CBS 5829;

MEDLINE-97412794; PubMed-9267437;

MEDLINE-97412794; PubMed-9267437;

Malone R.E., Pittnan D.L., Nau J.J.;

Malone R.E., Pittnan D.L., Nau J.J.;

Malone R.E., Pittnan D.L., Nau J.J.;

MERCI14 in Saccharomyces.";

Mol. Gen. Genet. 255:410-419(1997).

1- FUNCTION: REQUIRED FOR MEIOTIC RECOMBINATION EVENTS; NOT REQUIRED FOR MITOSIS.
                                                          PRINTS;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces paradoxus (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; DNA-directed RNA polymerase; Transcription;
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                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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-i- SUBCELLULAR LOCATION: Chloroplast.
-i- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                               EMBL; Y08767; CAA70020.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DEVELOPMENTAL STAGE: MEIOSIS-SPECIFIC
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                                                                                  PR01548; MEIOTICR114
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                                                                                                     IPR004354; Meiotic_rec114.
3525; Meiotic_rec114; 1.
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   432 AA;
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35, Last sequence 39, Last annotations.
                                                       Meiotic_rec114;
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   C53AF897B943075D CRC64;
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DR EMBL; AJ400840, ....

DR PIR; C2959; C29959; L1994.

DR HSSP, O9KW17; 1HOM.

DR Interpro, IPR001572; RNA_pol_B.

DR Pfam; PF04561; RNA_pol_Rpb2_1; 1.

DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.

DR Pfam; PF04562; RNA_pol_Rpb2_3; 1.

DR Pfam; PF04562; RNA_pol_Rpb2_6; 2.

DR Pfam; PF04560; RNA_pol_Rbb2_7; 1.

DR PF0517E; PS01166; RNA_pol_Rbb2_7; 1.

DR PROSITE; PS01166; RNA_POL_BETA; 1.

SEQUENCE 1070 AA; 120899 MW; 8BA809389B4A2IF9 CRC64;

SEQUENCE 1070 AA; 120899 MW; Score 37; DB 1; Length 1070;
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P11703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herrmann R.G., Mache R.;
"The plastid chromosome of spinach (Spinacia oleracea): complete nucleotide sequence and gene organization.";
plant Mol. Blob. 45:307-315(2001).
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-cv. Geant d'hiver, and cv.
MEDLINE-21187424, PubMed-11292076;
Schmitz-Linneweber C., Maier R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hudson G.S., Holton T.A., Whitfel "Spinach chloroplast rpoBC genes chloroplast RNA polymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=88316931;
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200:639-654(1988).
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on T.A., Whitfeld P.R.,
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Tracheophyta;

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RESULT 28

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01-NOV-1995 (Rel. 3
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MEDLINE=9535630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

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Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE-20137488; PubMed-1067502;
Langen H., Takacs B., Evers S., Berndt P.,
Gray C., Fountoulakis M.;
Two-dimensional map of the proteome of Hae
Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
Bacteria; Proteobacteria;
Pasteurellaceae; Haemophi
                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                   TIGR;
                                                                                                                                                                                                                                                                                                                                   EMBL; U32814; AAC22998.1; PIR; E64026; E64026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
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l; Mismatches
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38;
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AM3B_ORYSA
ID AM3B_O
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Best Local
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P27937;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: MONOMER:
-i- TISSUE SPECIFICITY: GERMINATING SEEDS.
-i- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
-i- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
-i- THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
-i- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-cv. Japonica M202; TISSUE-Etiolated leaf; MEDLINE-91329692; PubMed=1714318; Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.; "Characterization of an alpha-amylase multigene cluster in Plant Mol. Biol. 16:579-591(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucanohydrolase).
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01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006589; Alp_amyl.
InterPro; IPR006047; Alpha_am
Pfam; PF00128; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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HSSP; P04063; 1AVA.
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  (Rel.
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                                                                                                                                                                                                                                                                                                                     AA;
                                                           STANDARD;
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3C precursor (EC 3.2.
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precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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    sequence
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ALPHA-AMYLASE ISOZYME 3C.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMILARITY).
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CALCIUM (BY SIMILARITY).
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Pred. No.
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a; Poales; Poaceae;
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Alpha-amylase isozyme 3
glucanohydrolase).
AMY1.6 OR AMY3B.
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MEDLINE-91329692; PubMed-1714318;
Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
"Characterization of an alpha-amylase multigene cluster in rice.";
Plant Mol. Biol. 16:579-591(1991).
[2]
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InterPro; IPRO06047; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Anmy; 1.
Hydrolase; Glycosidase; Carbohydrate n
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERMINATION.

II CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

II COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

II SUBLNIT: MODOMET:

II TISSUB SPECIFICITY: GERMINATING SEEDS.

II DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SUBLILE T.D., Huang N., Rodriguez R.L.;
Subnitted (MAY-1989) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X56337; CAA39777.1; -. EMBL; M24941; AAA33897.1; -. PIR; S14957; S14957. PIR; S14957; PO4063; IAVA.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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ALPHA - ANYLASE ISOZYME 3B.

BY SIMILARITY.

BY SIMILARITY.

CALCIUM (BY SIMILARITY).

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CALCIUM (BY SIMILARITY).
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Copyright (c) 1993 - 2003 Compugen Ltd
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O812f3 plasmodium
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O41770 zea mays (m
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O91872 bacilius sp
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
Alpha-amylase subfamily Amyl protein (Fragment).
2 Alpha-amylase subfamily Amyl protein (Fragment).
3 Triticum aestivum (Wheat).
5 EuKaryota; Viridiplantae; Streptophyta; Embryophyta; Tebermatophyta; Magnollophyta; Liliopsida; Poales; Poac Triticeae; Triticum.
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MEDLINE-92366494; PubMed-1502164;

Huang N., Stebbins G.L., Rodriguez R.L.;

"Classification and evolution of alpha-amylase genes

"Classification and evolution of alpha-amylase genes

Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).

EMBL; S42213; AADI3822.1; -.

HSSP; P04063; 1AVA.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
Khursheed B., Rogers J.C.;
"Barley alpha-amylase genes. Quantitati
mRNA levels from individual members of
expressed in aleurone cells.";
J. Biol. Chem. 263:18953-18960(1988).
EMBL; J04202; AAA98615.1; -.
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01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Alpha-amylase precursor
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01-MAR-2003 (TrEMBLrel. )
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Q1-DEC-2001 (TrEMBLrel. 19, C
Q1-DEC-2001 (TrEMBLrel. 19, L
Q1-OCT-2002 (TrEMBLrel. 22, L
Putative alpha-amylase.
P0514H03.1 OR P0025H06.12.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Barley (H.vulgare) alpha-amylase 1.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embi
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006646; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
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SIGNAL 1 25
CHAIN 26 427
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Oryza sativa (Rice), and
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta;
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EMBL; M17125; AAA32926.1;
HSSP; P04063; IAVA.
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InterPro; IPR006599; Alp_amyl_cat_sub.
InterPro; IPR006599; Alp_amyl_cat_sub.
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                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 429;
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           Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes
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RESULT 5

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      RESULT 6
Q42504
ID Q425
AC Q425-
DT 01-N
DT 01-N
DT 01-M
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Best Local S
Matches 8
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Matches
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042365;
042365;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Alpha-amylase subfamily Amy2 protein (Fragment).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea;
Triticeae; Triticum.
    Q42504;
Q42504;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92366494; PubMed-1502164;
MEDLINE-92366494; PubMed-1502164;
Huang N., Stebbins G.L., Rodriguez R.L.;
Huang N., Stebbins G.L., Rodriguez R.L.;
**Classification and evolution of alpha-amylase genes
Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).
EMBL; $42217; AAD13823.1; -.
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0025H66.*;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003275; BAB63540.1; -.
EMBL; AP003312; BAC10723.1; -.
Gramene; 094DK9; -.
Gramene; 094DK9; -.
InterPro; IPR006047; Alpha-amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SEQUENCE 424 AA; 45862 MW; 228582D57B271692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=0.sativa (japonica cultivar-group);
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-O. sativa; STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0514H03.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; M
Ehrhartoideae; O
NCBI_TaxID=4530,
                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                          Match
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                                                                                                                                                                                                                                                    Similarity
8; Conserv
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8; Conservative
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    6 (TrEMBLrel.
6 (TrEMBLrel.
8 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                               29
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                                                                               PRELIMINARY;
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Oryzeae; Oryza.
), 39947;
                                                                                                                                                                                                                                                                                                                               3082 MW;
                                                                                                                                                                                                                                                                      85.7%;
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    01,
01,
23,
  Created)
Last sequence up
Last annotation
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Pred. No. 0.15;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                             71FB73013D584AA8 CRC64;
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Pred. No. 1
                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                               421
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1.1;
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    update)
on update)
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                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                     Length 29;
                                                                                                                                                                                                                                                    Indels
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Whittier R.F., Dean D.A., ROSS
Submitted (FEB-1991) to the EB
EMBL; M05166; CAA2803.1; -.
EMBL; M15208; AA32935.1; -.
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Whittier R.F., Dean Nucleic Acids Res. 1 [2]
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Matthews P.R., Gubler F., Jacobsen J.V.;
Matthews P.R., Gubler F., Jacobsen J.V.;
"A plant-based expression system for matching isozymes.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ EMBL; Y11726; CAA772143.1;
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 004964;
PRINTS; PRO0110: ALPHAAMYLASE
SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase,
SEQUENCE 437 AA; 47776 MW;
                                                                InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR0060589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; Pf00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-amylase (EC AMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
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AMY1 OR AMY32B.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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InterPro; IPR006048; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amylase multigene family in
gibberellic acid.";
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ROGERS J.C., Milliman C.;
"Coordinate increase in major transcripts from the high pI alpha-
"Coordinate increase in major transcripts from the high pI alpha-
"The particular in the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the
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NCBI_TaxID=4513;
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||||:|||:
53 VNWVDKVGGA 26:
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13:0-0(1987).
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he EMBL/GenBank/DDBJ
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    E163524C88CB2480 CRC64;
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HSSP; P04063; 1AVA.
InterPro; IPR006589; Alpha_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
SEQUENCE 437 AA; 47770 MW; 67E910E7(
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Q40017;
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-MAR-2003 (TrEMBLrel. 23,
Alpha-amylase (EC 3.2.1.1).
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Bukaryota; Viridiplantae; Streptophyta; Em
Eukaryota; Viridiplantae; Liliopsida;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Barley (H.vulgare) alpha-amylase 2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
Triticeae; Hordeum.
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    SMART;
                  InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub
Pfam; PF00128; alpha-amylase; 1.
                                                                         Plant Mol. Biol. 9:3-17(1987).
EMBL; M17128; AAA32927.1; -.
HSSP; P04063; 1AVA.
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Eukaryota; Viridiplantae; Streptopl Spermatophyta; Magnoliophyta; Lilic Triliceae, Hordeum.
                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Barley (H.vulgare) alpha-amylase 2.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Q40018;
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EMBL; M17126; AAA32925.1;
HSSP; P04063; 1AVA.
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EMBL; M17127; AAA32928.1; -
HSSP; P04063; 1AVA.
                                                                              SEQUENCE FROM N.A.
Knox C.A.P., Sonthayanon B.,
"Structure and organization
barley.";
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NCBI_TaxID=4513;
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InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAMYLASE.
SEQUENCE 427 AA; 47402 MW; D21BA
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01-MAR-2003 (TEMBLrel 23, L
01-MAR-2003 (TEMBLrel 23, L
01-MAR-2003 (TEMBLrel 23, L
Alpha-amylase precursor (EC 3
Musa acuminata (Banana).
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Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
Sequencing and molecular characterization of a banana alpha-amylase
CDNA clone related to the fruit ripening";
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AF533648; AAN01149.1;
InterPro; IPR0066047; Alpha_amyl_cat.
InterPro; IPR0065089; Alp_amyl_cat.
InterPro; IPR0065089; Alp.amyl_cat.
InterPro; IPR0065089; Alp.amyl_cat.
STATES; PR00110; ALPHAAMTLASE.
PRINTS; PR00112; ALPHAAMTLASE.
SMART; SM00642; AAmy; 1.
SMART; SM00642; AAmy; 1.
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01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1).
Musa acuminata (Banana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
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InterPro; IPR006046; Glyco_hydro_l3.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAWYLASE.
SMART; SM00642; Ammy; 1.
SMART; SM0642; Amy; 1.
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"Sequence and molecular characterization of the alpha-amylase expressed during maturation of the banana (Musa spp.).";
Thesis (2001), Universidade de Sao Paulo, Sao Paulo, Brasil.
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EMBL, AJ010728; CAA09323.1; -
HSSP, P04063; 1AVA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006589; Alpha_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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STRAIN-ev. Nanicao; TISSUE-Leaf;
Viaira A. Jr., Nascimento J.R.O., Lajolo F.
"Sequencing and molecular characterization"
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EMBL; AJ010729; CAA09324.1; -.
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InterPro; IPR006047; Alpha_amyl_cat.
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Afonso C.L., Tulman E.R., Lu Z., Z
Kerembekova U.Z., Sandybaev N.T.,
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Submitted (OCT-2001) to the EMBL/C
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Gubser C., Smith G.L.;
"The sequence of camelpox virus shows it
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J. Gen. virol. 83:855-872(2002).
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   Oberste M.S., Greenwood J.D., Gonda M.A.;
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J. Virol. 65:3932-3937(1991).
                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91251255; PubMed=1645801;
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NCBI_TaxID=11647;
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Viruses; Retroid viruses; Retroviridae;
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Putative 39.6k protein.
MVA185L.
                                                 STRAIN-Brighton Red;
MEDLINE-90177240; PubMed-2309453;
Parsons B.L., Pickup D.J.;
"Transcription of orthopoxvirus telomeres infection.";
                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALN=Brighton Red;
STRALN=B3117629; pubMed=6961398;
MEDLINE=8317629; pubMed=6961398;
Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
"Sequence of terminal regions of cowpox virus DNA:
repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
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01-JUN-2002
01-JUN-2002
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SEQUENCE 340 AA; 39566 MW; DA944A21A712FFB7 CRC64;
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    Virology 175:69-80(1990) [3]
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Viruses; dsDNA viruses,
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"The complete genomic sequen
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Dietrich F.S., Ray C.,
Submitted (FEB-2002) t
EMBL; AF482758; AAM136
SEQUENCE 340 AA; 39
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072752;
01-AUG-1998
01-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus (CPV).
Viruses; dsDNA viruses,
Orthopoxvirus.
NCBI_TaxID=10243;
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MEDLINE-94378510; PubMed-8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
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B15L.
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Pickup D.J.;
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STRALN-Brighton Red;
MEDLINE-90196263; PubMed-2014645;
MEDLINE-90196263; PubMed-2014645;
"Transcription of the terminal loop reinitiated from the telomere sequences virology 181:716-720(1991).
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AAM13649.1; .
AA, 39662 MW; A13AECFF851CFF62 CRC64;
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EMBL; AF012825; AAC99569.1; -. SEQUENCE 340 AA; 39636 MW; 294147
                                                                        Q65597; PRELIMINARY;
Q65597; 01-NOV-1996 (TrEMBLrel. 0
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Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng
Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
"Complete genomic sequence of vaccinia virus (
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
EMBL; AF095689; AAF34088.1; -
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RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

ADDMann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

AJ Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

AM Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

AN Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

REJEL, AL596170; CAC97247.1; ".
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InterPro: IPR002114; HPr_SerP_Site.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA;
PROSITE; PS00559; PTS_HPR_SER; 1.
SEQUENCE 875 AA; 99108 MW; 0FA8D362
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RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
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RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L., Maitournam A., Mata Vicente J., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R.,
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RRA Nordsiek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R.,
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RRA Vazquez-Boland J.-A., Contest P.,
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01-NOV-1999 (TYEMBLEEL 12, Las
01-MAR-2003 (TYEMBLEEL 23, Las
Hypothetical protein APE0774.
APE0774
                                                                                                                                          Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K., Kudoh Y., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Kubota K., "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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01-MAR-2003 (TrEMBLrel. 23, I
Hypothetical protein lmo1903.
LMO1903.
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Archaea; Crenarchaeota;
Desulfurococcaceae; Aero
NCBI_TaxID=56636;
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ICEF-II ORF17 (Fragment).
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Q8ZX92;
01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                 MEDILINE=22336318; PubMed=12446643; Calcutt M.J., Lewis M.S., Wise K.S.; "Molecular Genetic Analysis of ICEF, an I That Is Present as a Repetitive Sequence Mycoplasma fermentans PG18."; Bacteriol. 184.6929-6941(2002).

EMBL. AY168965; AAN85277.1; -. NON_TER
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Mycoplasma fermentans.

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

NCBI_TaxID=2115;
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EMBL, AE009819; AAL63457.1; .
InterPro; IPR002965; Prich extensn.
PRINTS; PRO1217; PRICHEXTENSN.
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STRAIN-IM2 / AFCC 51768 / DSM 7523;
PubMed-11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O.,
Miller J.H.;
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NCBI_TaxID=13773;
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Archaea: Crenarchaeota;
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RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., CChetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Charbit A., Chetouani F., Couve E., Hain T., Barrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RC Comparative genomics of Listeria species.";
RC Science 294.849-852(2001).
RR RA M2591978; CAC99332.1; -.
DR ListiList; LM001254; -.
DR ListiList; LM001254; -.
DR InterPro; IPR006089; Alp_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
KW Hypothetical protein; Complete proteome.
SART; SM00642; Aamy; 1.
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Best Local
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O8Y7MO PRELIMINARY; PRT; 548 AA. 08Y7MO; 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein lmo1254.
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firm.cutes; Bacillales; Listeriaceae; Listeria.
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124 VKWANKMGG 132
                                                                              137 NWVSKFGGN 145
                                                                                                                      2 NWVNKVGGS 10
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                                                                                                                                                                              Similarity
                                                                                                                                                             Conservative
                                                                                                                                                       69.6%; Score 39; DB 16; Length 548; 66.7%; Pred. No. 1.3e+02; tive 2; Mismatches 1; Indels
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